

**METHODS AND NUCLEIC ACIDS FOR THE ANALYSIS OF GENE EXPRESSION
ASSOCIATED WITH THE DEVELOPMENT OF PROSTATE CELL
PROLIFERATIVE DISORDERS**

FIELD OF THE INVENTION

5 The present invention relates to human DNA sequences that exhibit altered heterogenous expression patterns in prostate cancer patients. Particular embodiments of the invention provide methods for the diagnosis of individuals with said disorder.

CROSS-REFERENCE TO RELATED APPLICATIONS

10 This application claims the benefit of priority to the following applications: European application number 03090414.8, filed 01 December 2003; European application number 04090040.9, filed 10 February 2004; European application number 04090187.8, filed 10 May 2004; and European application number 04090292.6, filed 21 July 2004; all of which are incorporated by reference herein in their entireties.

SEQUENCE LISTING

15 A Sequence Listing, pursuant to 37 C.F.R. § 1.52(e)(5), has been provided on compact disc (1 of 1) as a 1.64 MB text file, entitled "47675-95 Sequence Listing.txt," and which is incorporated by reference herein in its entirety.

BACKGROUND

20 *Correlation of aberrant DNA methylation with cancer.* Aberrant DNA methylation within CpG 'islands' is characterized by *hyper-* or *hypomethylation* of CpG dinucleotide sequences leading to abrogation or over expression of a broad spectrum of genes, and is among
25 the earliest and most common alterations found in, and correlated with human malignancies. Additionally, abnormal methylation has been shown to occur in CpG-rich regulatory elements in both intronic and coding parts of genes for certain tumors. In colon cancer, aberrant DNA methylation constitutes one of the most prominent alterations and inactivates many tumor suppressor genes including, *inter alia*, p14ARF, p16INK4a, THBS1, MINT2, and MINT31 and
30 DNA mismatch repair genes such as hMLH1.

 Aside from the specific hypermethylation of tumor suppressor genes, an overall hypomethylation of DNA can be observed in tumor cells. This decrease in global methylation can be detected early, far before the development of frank tumor formation. A correlation

between hypomethylation and increased gene expression has been determined for many oncogenes.

Prostate cancer. Prostate cancer is the most common malignancy among men in the United States (~200,000 new cases per year), and the sixth leading cause of male cancer-related deaths worldwide (~204,000 per year). Prostate cancer is primarily a disease of the elderly, with approximately 16% of men between the ages of 60 and 79 having the disease. According to some estimates at autopsy, 80% of all men over 80 years of age have some form of prostate disease (eg cancer, BPH, prostatitis, etc). Benign prostate hypertrophy is present in about 50% of men aged 50 or above, and in 95% of men aged 75 or above. It is obvious from these reports that prostate cancer is often not a disease that men die from, but with. Recent evidence suggests that the incidence of prostate cancer may in fact be declining, likely as result of better treatment, better surgery, and earlier detection.

Diagnosis of prostate cancer; molecular approaches. Current guidelines for prostate cancer screening have been suggested by the American Cancer Society and are as follows: At 50 years of age, health care professionals should offer a blood test for prostate specific antigen (PSA) and perform a digital rectal exam (DRE). It is recommended that high risk populations, such as African Americans and those with a family history of prostate disease, should begin screening at 45 years of age. Men without abnormal prostate pathology generally have a PSA level in blood below 4ng/ml. PSA levels between 4ng/ml and 10ng/ml (called the 'grey zone') have a 25% chance of having prostate cancer. The result is that 75% of the time, men with an abnormal DRE and a PSA in this grey zone have a negative, or a seemingly unnecessary biopsy. Above the *grey zone*, the likelihood of having prostate cancer is significant (> 67%) and increases even further as PSA levels go up. Numerous methods exist for measuring PSA (percent-free PSA, PSA velocity, PSA density, etc.), and each has an associated accuracy for detecting the presence of cancer. Yet, even with the minor improvements in detection, and the reported drops in mortality associated with screening, the frequency of false positives remains high. Reduced specificity results in part from increased blood PSA associated with BPH, and prostatitis. It has also been estimated that up to 45% of prostate biopsies under current guidelines are falsely negative, resulting in decreased sensitivity even with biopsy.

TRUS guided biopsy is considered the 'gold standard' for diagnosing prostate cancer. Recommendations for biopsy are based upon abnormal PSA levels and/or an abnormal DRE. For PSA, there is a grey zone where a high percentage of biopsies are perhaps not necessary. Yet the ability to detect cancer in this grey zone (PSA levels of 4.0 to 10 ng/ml) is difficult without biopsy. Due to this lack of specificity, 75% of men undergoing a biopsy do not have

cancer. Yet without biopsy, those with cancer would be missed, resulting in increased morbidity and mortality. Unfortunately, the risks associated with an unnecessary biopsy are also high.

Molecular markers would offer the advantage that they can be used to efficiently analyze even very small tissue samples, and samples whose tissue architecture has not been maintained.

5 Within the last decade, numerous genes have been studied with respect to differential expression among benign hyperplasia of the prostate and different grades of prostate cancer. However, no single marker has as yet been shown to be sufficient for the detection of prostate tumors in a clinical setting.

Alternatively, high-dimensional mRNA-based approaches may, in particular instances, 10 provide a means to distinguish between different tumor types and benign and malignant lesions. However, application of such approaches as a routine diagnostic tool in a clinical environment is impeded and substantially limited by the extreme instability of mRNA, the rapidly occurring expression changes following certain triggers (*e.g.*, sample collection), and, most importantly, by the large amount of mRNA needed for analysis which often cannot be obtained from a 15 routine biopsy (see, *e.g.*, Lipshutz, R. J. et al., *Nature Genetics* 21:20-24, 1999; Bowtell, D. D. L. *Nature Genetics Suppl.* 21:25-32, 1999).

Aberrant genetic methylation in prostate cancer has been observed in several genes including Gstp1, AR, p16 (CDKN2a/INK4a), CD44, CDH1. Genome-wide hypomethylation for example of the LINE-1 repetitive element has also been associated with tumor progression 20 (Santourlidis, S., et al., *Prostate* 39:166-74, 1999).

Prostate cancer methylation markers. The core promoter region of the Gluthione S-Transferase P gene (GSTP1; accession no. NM_000852) has been shown to be hypermethylated in prostate tumor tissue. The glutathione S-transferase pi enzyme is involved in the detoxification of electrophilic carcinogens, and impaired or decreased levels of enzymatic 25 activity (GSTP1 impairment) have been associated with the development of neoplasms, particularly in the prostate. Mechanisms of GSTP1 impairment include mutation (the GSTP*B allele has been associated with a higher risk of cancer) and methylation. However, with respect to the use of Gstp1 markers, the prior art is limited with respect to the number of Gstp1 promoter CpG sequences that have been characterized for differential methylation status. Moreover, there 30 are no disclosures, suggestions or teachings in the prior art of how such markers could be used to distinguish among benign hyperplasia of the prostate and different grades of prostate cancer.

Aberrant genetic methylation has also been observed in several other genes including AR, p16 (CDKN2a/INK4a), CD44, CDH1. Genome-wide hypomethylation, for example, of the

LINE-1 repetitive element has also been associated with tumor progression (Santourlidis, S., et al., *Prostate* 39:166-74, 1999).

However, use of these genes as alternative or supplemental diagnostically or otherwise clinically useful markers in a commercial setting has not been enabled. The application of differentially methylated genes to clinically utilizable platforms requires much further investigation into the sensitivity and specificity of the genes. For example, in the case of the gene CD44, a known metastasis suppressor, downregulation was associated with hypermethylation. However the use of this gene as a commercially available marker was not enabled, because it was also methylated in normal tissues (*see* Vis, et al., *Mol Urol.* 5:199-203, 2001).

Development of medical tests. Two key evaluative measures of any medical screening or diagnostic test are its *sensitivity* and *specificity*, which measure how well the test performs to accurately detect all affected individuals without exception, and without falsely including individuals who do not have the target disease (predictive value). Historically, many diagnostic tests have been criticized due to poor *sensitivity* and *specificity*. A true positive (TP) result is where the test is positive and the condition is present. A false positive (FP) result is where the test is positive but the condition is not present. A true negative (TN) result is where the test is negative and the condition is not present. A false negative (FN) result is where the test is negative but the condition is not present.

In this context: Sensitivity = $TP/(TP+FN)$; Specificity = $TN/(FP+TN)$; and Predictive value = $TP/(TP+FP)$.

Sensitivity is a measure of a test's ability to correctly detect the target disease in an individual being tested. A test having poor sensitivity produces a high rate of false negatives, *i.e.*, individuals who have the disease but are falsely identified as being free of that particular disease. The potential danger of a false negative is that the diseased individual will remain undiagnosed and untreated for some period of time, during which the disease may progress to a later stage wherein treatments, if any, may be less effective. An example of a test that has low sensitivity is a protein-based blood test for HIV. This type of test exhibits poor sensitivity because it fails to detect the presence of the virus until the disease is well established and the virus has invaded the bloodstream in substantial numbers. In contrast, an example of a test that has high sensitivity is viral-load detection using the polymerase chain reaction (PCR). High sensitivity is achieved because this type of test can detect very small quantities of the virus. High sensitivity is particularly important when the consequences of missing a diagnosis are high.

Specificity, on the other hand, is a measure of a test's ability to identify accurately patients who are free of the disease state. A test having poor specificity produces a high rate of false positives, i.e., individuals who are falsely identified as having the disease. A drawback of false positives is that they force patients to undergo unnecessary medical procedures treatments with their attendant risks, emotional and financial stresses, and which could have adverse effects on the patient's health. A feature of diseases which makes it difficult to develop diagnostic tests with high specificity is that disease mechanisms, particularly in cancer, often involve a plurality of genes and proteins. Additionally, certain proteins may be elevated for reasons unrelated to a disease state. An example of a test that has high specificity is a gene-based test that can detect a p53 mutation. Specificity is important when the cost or risk associated with further diagnostic procedures or further medical intervention are very high.

The PSA blood test has a sensitivity of 73%, specificity of 60% and predictive value of 31.5%. PSA sensitivity and specificity can be improved but involve tradeoffs. PSA sensitivity can be improved by adjusting the "normal" PSA level to a lower value for younger men or by following serum PSA values in an individual patient over time (PSA velocity). Both methods will increase the number of cancers detected, but they also increase the number of men undergoing biopsy. Conversely, specificity can be improved by using higher "normal" PSA levels for older men, by using the free-to-total PSA ratio, or by adjusting the normal value according to the size of the prostate. These three methods decrease the number of unnecessary biopsies, but they increase the risk that some cancers will be missed.

It can therefore be seen that there exists a need for a means of prostate cancer diagnosis with improved sensitivity, specificity and/or predictive value.

Sensitivity and specificity of quantitative methylation-specific polymerase chain reaction (QMSP) assay alone (without histological analysis) in prostate cancer analysis of needle biopsies has ranged from 30% sensitivity and 100% specificity to 89% sensitivity and 64% specificity (Harden *et. al.* J Natl Cancer Inst 2003; 95: 1634-1637). However the predictive value of said technique as a clinical screening tool was not analysed. Furthermore, genetic testing of serum and bodily fluids such as urine and saliva would reduce the need for biopsies to detect cancer and would thus be the most effective screening or monitoring tool. However the development of such tests requires an extremely high degree of sensitivity and specificity. Analysis of Gstp1 gene hypermethylation (Cairns P, et al. *Clin Cancer Res* 7:2727-30 2001.) in urine sediment of prostate cancer patients showed that only 6 out of 22 individuals with elevated methylation levels in biopsied tumors showed corresponding hypermethylation in urine samples.

Multifactorial approach. Cancer diagnostics has traditionally relied upon the detection of single molecular markers (e.g. gene mutations, elevated PSA levels). Unfortunately, cancer is a disease state in which single markers have typically failed to detect or differentiate many forms of the disease. Thus, assays that recognize only a single marker have been shown to be of limited predictive value. A fundamental aspect of this invention is that methylation based cancer diagnostics and the screening, diagnosis, and therapeutic monitoring of such diseases will provide significant improvements over the state-of-the-art that uses single marker analyses by the use of a selection of multiple markers. The multiplexed analytical approach is particularly well suited for cancer diagnostics since cancer is not a simple disease, this multi-factorial “panel” approach is consistent with the heterogeneous nature of cancer, both cytologically and clinically.

Pronounced need in the art. Therefore, in view of the incidence of prostate hyperplasia (50% of men aged 50 or above, and 95% of men aged 75 or above) and prostate cancer (180 per 100,000), there is a substantial need in the art for the development of molecular markers that could be used to provide sensitive, accurate and non-invasive methods (as opposed to, e.g., biopsy and transrectal ultrasound) for the screening of populations to provide an early diagnosis of prostate cell proliferative disorders.

SUMMARY OF THE INVENTION

The present invention provides novel methods and nucleic acids for the detection of and/or differentiation between prostate cell proliferative disorders. The invention thereby addresses the longfelt need for novel means for the early diagnosis of prostate cell proliferative disorders, in particular for the detection of prostate cancer, prostate carcinoma and prostate neoplasms.

The invention solves this longstanding need in the art by providing a panel of genes, genomic sequences and/or regulatory regions thereof according to Table 26, the expression levels thereof being indicative of the presence of prostate cell proliferative disorders or features thereof. In particular the methylation status of CpG positions thereof are indicative of the presence of prostate cell proliferative disorders or features thereof. Preferred selections and combinations of genes are provided, the methylation analysis of which enable the detection of prostate cell proliferative disorders.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1,

PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER
 PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ
 ID NO: 11, SEQ ID NO: 1028, LIM/HOMEOBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ
 ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED
 5 MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most
 preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said
 genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting
 of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate
 10 cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or
 neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or
 neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly
 preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one
 15 or more genes and/or sequences selected from Table 26 are analysed. It is also preferred that
 SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting
 GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC
 FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR
 NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEOBOX PROTEIN LHX9, SEQ ID
 20 NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED
 MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are
 analysed.

Particularly preferred are the combinations of genes described in Tables 22 and 23, in
 particular the analysis of SEQ ID NO: 1023 and GSTP1.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from
 prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes
 under stringent conditions to, one or more more sequences comprising at least 16 contiguous
 nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at
 least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue
 from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly
 preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or
 more more sequences comprising at least 16 contiguous nucleotides of the sequences according

to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

It is particularly preferred that said prostate cell proliferative disorder is a prostate cancer, prostate carcinoma or prostate neoplasm. In further embodiments the invention provides methods and nucleic acids for the differentiation between non-cancerous types of prostate tissue (including BPH and normal) from prostate carcinoma. In further embodiments the invention provides methods and nucleic acids for the differentiation of prostate cancer from normal prostate tissue, tissues originating from other tissues and BPH. In further embodiments the invention provides methods and nucleic acids for the differentiation of prostate cancer from cancers originating from other tissues.

In order to enable this analysis the invention provides a method for the analysis of biological samples for genomic methylation associated with the development of prostate cell proliferative disorders. Said method is characterised in that at least one nucleic acid, or a fragment thereof, from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 is/are contacted with a reagent or series of reagents capable of distinguishing between methylated and non methylated CpG dinucleotides within the genomic sequence, or sequences of interest. It is further preferred that at least one nucleic acid, or a fragment thereof, from the group consisting of SEQ ID NO: 1023, SEQ ID NO: 57, SEQ ID NO: 20, SEQ ID NO: 36, SEQ ID NO: 1171, SEQ ID NO: 51, SEQ ID NO: 31, SEQ ID NO: 24, SEQ ID NO: 11, SEQ ID NO: 1028, SEQ ID NO: 4, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, SEQ ID NO: 18, SEQ ID NO: 1019 and SEQ ID NO: 1027 is/are contacted with a reagent or series of reagents capable of distinguishing between methylated and non methylated CpG dinucleotides within the genomic sequence, or sequences of interest.

It is particularly preferred that the method and nucleic acids according to the invention are utilised for at least one of: detection of; screening of populations for; differentiation between; monitoring of; and detection and monitoring of prostate cell proliferative disorders.

The present invention provides a method for ascertaining genetic and/or epigenetic parameters of genomic DNA. The method has utility for the improved detection of and/or

differentiation between prostate cell proliferative disorders. The invention presents several improvements over the state of the art. Although methylation assays for the detection of prostate cancer are known there is currently no molecular classification system for the detection of prostate cell proliferative disorders, nor one that accurately differentiates benign conditions from prostate carcinomas and neoplasms.

The source may be any suitable source. Preferably, the source of the DNA sample is selected from the group consisting of cells or cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof. Preferably, the source is biopsies, bodily fluids, ejaculate, urine, or blood.

Specifically, the present invention provides a method for the detection of prostate cell proliferative disorders, comprising: obtaining a biological sample comprising genomic nucleic acid(s); contacting the nucleic acid(s), or a fragment thereof, with one reagent or a plurality of reagents sufficient for distinguishing between methylated and non methylated CpG dinucleotide sequences within a target sequence of the subject nucleic acid, wherein the target sequence comprises, or hybridizes under stringent conditions to, a sequence comprising at least 16 contiguous nucleotides of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171, said contiguous nucleotides comprising at least one CpG dinucleotide sequence; and determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences.

It is particularly preferred that the target sequence comprises, or hybridizes under stringent conditions to, a sequence comprising at least 16 contiguous nucleotides of SEQ ID NO: 1023, SEQ ID NO: 57, SEQ ID NO: 20, SEQ ID NO: 36, SEQ ID NO: 1171, SEQ ID NO: 51, SEQ ID NO: 31, SEQ ID NO: 24, SEQ ID NO: 11, SEQ ID NO: 1028, SEQ ID NO: 4, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, SEQ ID NO: 18, SEQ ID NO: 1019 and SEQ ID NO: 1027 said contiguous nucleotides comprising at least one CpG dinucleotide sequence; and determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences.

Preferably, distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises methylation state-dependent conversion or non-conversion of at least one such CpG dinucleotide sequence to the corresponding converted or non-converted dinucleotide sequence within a sequence selected from the group consisting of

SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 , and contiguous regions thereof corresponding to the target sequence.

Additional embodiments provide a method for the detection of and/or differentiation between prostate cell proliferative disorders, comprising: obtaining a biological sample having
5 subject genomic DNA; extracting the genomic DNA; treating the genomic DNA, or a fragment thereof, with one or more reagents to convert 5-position unmethylated cytosine bases to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties; contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence at least 9
10 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 , and complements thereof, wherein the treated DNA or the fragment thereof is either amplified to produce an amplificate, or is not amplified; and determining, based on a presence or absence of, or on a property of said amplificate, the
15 methylation state of at least one CpG dinucleotide sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 , or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences thereof. Preferably, at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase. Preferably,
20 determining comprises use of at least one method selected from the group consisting of: hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 , and complements thereof; hybridizing at least one
25 nucleic acid molecule, bound to a solid phase, comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 , and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is
30 complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 , and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing of the amplificate.

Further embodiments provide a method for the detection of and/or differentiation between prostate cell proliferative disorders, comprising: obtaining a biological sample having subject genomic DNA; extracting the genomic DNA; contacting the genomic DNA, or a fragment thereof, comprising one or more sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 or a sequence that hybridizes under stringent conditions thereto, with one or more methylation-sensitive restriction enzymes, wherein the genomic DNA is either digested thereby to produce digestion fragments, or is not digested thereby; and determining, based on a presence or absence of, or on property of at least one such fragment, the methylation state of at least one CpG dinucleotide sequence of one or more sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences thereof. Preferably, the digested or undigested genomic DNA is amplified prior to said determining.

Additional embodiments provide novel genomic and chemically modified nucleic acid sequences, as well as oligonucleotides and/or PNA-oligomers for analysis of cytosine methylation patterns within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1 to 3 show ranked matrices produced from bisulfite sequencing data. The overall matrix represents the sequencing data for one fragment. Each row of the matrix represents a single CpG site within the fragment and each column represents an individual sample. The bar on the left represents a scale of the percent of methylation, with the degree of methylation represented by the shade of each position within the column from black representing 100% methylation to light grey representing 0% methylation. No data was available at white positions.

Figure 1 shows the sequencing data of a fragment of the gene Prostaglandin E2 Receptor, EP4 Subtype wherein the sequenced samples are from prostate carcinoma.

Figure 2 shows the sequencing data of a fragment of the gene Orphan Nuclear Receptor (a-1Fetoprotein Transcription Factor wherein the sequenced samples are from prostate carcinoma.

Figure 3 shows the sequencing data of a fragment of the gene 1-Acyl-SN-Glycerol-3-Phosphate Acyltransferase Gamma wherein the sequenced samples are from prostate carcinoma.

Figure 4 shows Normal prostate and BPH vs. Prostate Cancer marker rankings according to Example 3. Each individual genomic region of interest is represented as a point. The left plot gives uncorrected p-values from the genewise logistic regression model. Lower and upper dotted lines show 5% Bonferroni and FDR limits respectively. The X-axis shows the p values for the individual CpG positions. The p values are the probabilities that the observed distribution occurred by chance in the data set. The right plot gives accuracy, sensitivity and specificity of a linear SVM trained on methylation measurements from all oligonucleotides. The accuracy of each genomic region is represented as black squares, the specificity as unfilled diamonds, the sensitivity as unfilled squares. The accuracy as measured on the X-axis shows the fraction of correctly classified samples.

Figure 5 shows the best 12 markers for Normal prostate and BPH vs. Prostate Cancer differentiation according to Example 3. Normal prostate and BPH samples are shown on the left. Prostate cancer is on the right. Each column represents one sample; each row one oligonucleotide. Oligonucleotides are grouped by candidate marker. The indicated markers are ordered from top to bottom with increasing accuracy. On the right side of each marker, Bonferroni corrected p-values are listed. Methylation data are centered and normalized to one standard deviation for individual oligonucleotides. The color represents the relative distance of the oligonucleotide methylation status from the mean value. Green color represents hypomethylated CpGs within an oligonucleotide while red indicates hypermethylated CpGs within an oligonucleotide.

Figure 6 shows Normal Prostate, BPH and Other Tissues vs. Prostate Cancer marker rankings according to Example 3. Each individual genomic region of interest is represented as a point. The left plot gives uncorrected p-values from the genewise logistic regression model. Lower and upper dotted lines show 5% Bonferroni and FDR limits respectively. The X-axis shows the p values for the individual CpG positions. The p values are the probabilities that the observed distribution occurred by chance in the data set. The right plot shows accuracy, sensitivity and specificity of a linear SVM trained on methylation measurements from all oligonucleotides. The accuracy of each genomic region is represented as black squares, the specificity as unfilled diamonds, the sensitivity as unfilled squares. The accuracy as measured on the X-axis shows the fraction of correctly classified samples.

Figure 7 shows the best 12 markers for Normal Prostate, BPH and Other Tissues vs. Prostate Cancer differentiation according to Example 3. Normal Prostate, BPH and Other Tissues samples are shown on the left. The 'Other Tissues' included normal tissue from other organs and cancer of other origins than prostate, according to table 7. Prostate cancer is on the

right. Each column represents one sample; each row one oligonucleotide. Oligonucleotides are grouped by candidate marker. The indicated markers are ordered from top to bottom with increasing accuracy. On the right side of each marker, Bonferroni corrected p-values are listed. Methylation data are centered and normalized to one standard deviation for individual
 5 oligonucleotides. The color represents the relative distance of the oligonucleotide methylation status from the mean value. Green color represents hypomethylated CpGs within an oligonucleotide while red indicates hypermethylated CpGs within an oligonucleotide.

Figure 8 shows Normal Prostate, BPH and Other Tissues vs. Prostate Cancer marker rankings according to Example 3. Each individual genomic region of interest is represented as a
 10 point. The left plot gives uncorrected p-values from the genewise logistic regression model. Lower and upper dotted lines show 5% Bonferroni and FDR limits respectively. The X-axis shows the p values for the individual CpG positions. The p values are the probabilities that the observed distribution occurred by chance in the data set. The following cancers are shown from left to right: bladder, melanoma, testes, kidney, endometrial cancer, lung, breast, pancreatic,
 15 liver, ovarian, salivary gland, and prostate.

DETAILED DESCRIPTION OF THE INVENTION

Definitions:

As used herein the term expression shall be taken to mean the transcription and
 20 translation of a gene. The level of expression of a gene may be determined by the analysis of any factors associated with or indicative of the level of transcription and translation of a gene including but not limited to methylation analysis, loss of heterozygosity (hereinafter also referred to as LOH), RNA expression levels and protein expression levels.

Furthermore the activity of the transcribed gene may be affected by genetic variations
 25 such as but not limited genetic mutations (including but not limited to SNPs, point mutations, deletions, insertions, repeat length, rearrangements and other polymorphisms).

The term "Observed/Expected Ratio" ("O/E Ratio") refers to the frequency of CpG dinucleotides within a particular DNA sequence, and corresponds to the [number of CpG sites / (number of C bases x number of G bases)].

30 The term "CpG island" refers to a contiguous region of genomic DNA that satisfies the criteria of (1) having a frequency of CpG dinucleotides corresponding to an "Observed/Expected Ratio" >0.6, and (2) having a "GC Content" >0.5. CpG islands are typically, but not always, between about 0.2 to about 1 kb, or to about 2kb in length.

The term “methylation state” or “methylation status” refers to the presence or absence of 5-methylcytosine (“5-mCyt”) at one or a plurality of CpG dinucleotides within a DNA sequence. Methylation states at one or more particular CpG methylation sites (each having two CpG CpG dinucleotide sequences) within a DNA sequence include “unmethylated,” “fully-methylated” and “hemi-methylated.”

The term “hemi-methylation” or “hemimethylation” refers to the methylation state of a palindromic CpG methylation site, where only a single cytosine in one of the two CpG dinucleotide sequences of the palindromic CpG methylation site is methylated (e.g., 5'-CC^MGG-3' (top strand): 3'-GGCC-5' (bottom strand)).

The term ‘AUC’ as used herein is an abbreviation for the area under a curve. In particular it refers to the area under a Receiver Operating Characteristic (ROC) curve. The ROC curve is a plot of the true positive rate against the false positive rate for the different possible cutpoints of a diagnostic test. It shows the tradeoff between sensitivity and specificity depending on the selected cutpoint (any increase in sensitivity will be accompanied by a decrease in specificity). The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test (the larger the area the better, optimum is 1, a random test would have a ROC curve lying on the diagonal with an area of 0.5; for reference: J.P. Egan. Signal Detection Theory and ROC Analysis, Academic Press, New York, 1975).

The term “hypermethylation” refers to the average methylation state corresponding to an *increased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

The term “hypomethylation” refers to the average methylation state corresponding to a *decreased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

The term “microarray” refers broadly to both “DNA microarrays,” and ‘DNA chip(s),’ as recognized in the art, encompasses all art-recognized solid supports, and encompasses all methods for affixing nucleic acid molecules thereto or synthesis of nucleic acids thereon.

“Genetic parameters” are mutations and polymorphisms of genes and sequences further required for their regulation. To be designated as mutations are, in particular, insertions, deletions, point mutations, inversions and polymorphisms and, particularly preferred, SNPs (single nucleotide polymorphisms).

“Epigenetic parameters” are, in particular, cytosine methylations. Further epigenetic parameters include, for example, the acetylation of histones which, however, cannot be directly analyzed using the described method but which, in turn, correlate with the DNA methylation.

The term “bisulfite reagent” refers to a reagent comprising bisulfite, disulfite, hydrogen sulfite or combinations thereof, useful as disclosed herein to distinguish between methylated and unmethylated CpG dinucleotide sequences.

The term “Methylation assay” refers to any assay for determining the methylation state of one or more CpG dinucleotide sequences within a sequence of DNA.

The term “MS.AP-PCR” (Methylation-Sensitive Arbitrarily-Primed Polymerase Chain Reaction) refers to the art-recognized technology that allows for a global scan of the genome using CG-rich primers to focus on the regions most likely to contain CpG dinucleotides, and described by Gonzalgo et al., *Cancer Research* 57:594-599, 1997.

The term “MethyLight™” refers to the art-recognized fluorescence-based real-time PCR technique described by Eads et al., *Cancer Res.* 59:2302-2306, 1999.

The term “HeavyMethyl™” assay, in the embodiment thereof implemented herein, refers to an assay, wherein methylation specific *blocking* probes (also referred to herein as *blockers*) covering CpG positions between, or covered by the amplification primers enable methylation-specific selective amplification of a nucleic acid sample.

The term “HeavyMethyl™ MethyLight™” assay, in the embodiment thereof implemented herein, refers to a HeavyMethyl™ MethyLight™ assay, which is a variation of the MethyLight™ assay, wherein the MethyLight™ assay is combined with methylation specific *blocking* probes covering CpG positions between the amplification primers.

The term “Ms-SNuPE” (Methylation-sensitive Single Nucleotide Primer Extension) refers to the art-recognized assay described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

The term “MSP” (Methylation-specific PCR) refers to the art-recognized methylation assay described by Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996, and by US Patent No. 5,786,146.

The term “COBRA” (Combined Bisulfite Restriction Analysis) refers to the art-recognized methylation assay described by Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997.

The term “MCA” (Methylated CpG Island Amplification) refers to the methylation assay described by Toyota et al., *Cancer Res.* 59:2307-12, 1999, and in WO 00/26401A1.

The term "hybridization" is to be understood as a bond of an oligonucleotide to a complementary sequence along the lines of the Watson-Crick base pairings in the sample DNA, forming a duplex structure.

5 "Stringent hybridization conditions," as defined herein, involve hybridizing at 68°C in 5x SSC/5x Denhardt's solution/1.0% SDS, and washing in 0.2x SSC/0.1% SDS at room temperature, or involve the art-recognized equivalent thereof (e.g., conditions in which a hybridization is carried out at 60°C in 2.5 x SSC buffer, followed by several washing steps at 37°C in a low buffer concentration, and remains stable). Moderately stringent conditions, as defined herein, involve including washing in 3x SSC at 42°C, or the art-recognized equivalent
10 thereof. The parameters of salt concentration and temperature can be varied to achieve the optimal level of identity between the probe and the target nucleic acid. Guidance regarding such conditions is available in the art, for example, by Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, N.Y.; and Ausubel et al. (eds.), 1995, Current Protocols in Molecular Biology, (John Wiley & Sons, N.Y.) at Unit 2.10.

15 The terms "array SEQ ID NO," "composite array SEQ ID NO," or "composite array sequence" refer to a sequence, hypothetical or otherwise, consisting of a head-to-tail (5' to 3') linear composite of all individual contiguous sequences of a subject array (e.g., a head-to-tail composite of SEQ ID NO:1-71, in that order).

The terms "array SEQ ID NO node," "composite array SEQ ID NO node," or "composite
20 array sequence node" refer to a *junction* between any two individual contiguous sequences of the "array SEQ ID NO," the "composite array SEQ ID NO," or the "composite array sequence."

In reference to composite array sequences, the phrase "contiguous nucleotides" refers to a contiguous sequence region of any individual contiguous sequence of the composite array, but does not include a region of the composite array sequence that includes a "node," as defined
25 herein above.

Overview:

The present invention provides molecular genetic markers that have novel utility for the detection of and/or differentiation between prostate cell proliferative disorders. It is particularly
30 preferred that the method and nucleic acids according to the invention are utilised for at least one of: detection of; screening of populations for; differentiation between; monitoring of; and detection and monitoring of prostate cell proliferative disorders.

Bisulfite modification of DNA is an art-recognized tool used to assess CpG methylation status. 5-methylcytosine is the most frequent covalent base modification in the DNA of eukaryotic cells. It plays a role, for example, in the regulation of the transcription, in genetic imprinting, and in tumorigenesis. Therefore, the identification of 5-methylcytosine as a component of genetic information is of considerable interest. However, 5-methylcytosine positions cannot be identified by sequencing, because 5-methylcytosine has the same base pairing behavior as cytosine. Moreover, the epigenetic information carried by 5-methylcytosine is completely lost during, e.g., PCR amplification.

The most frequently used method for analyzing DNA for the presence of 5-methylcytosine is based upon the specific reaction of bisulfite with cytosine whereby, upon subsequent alkaline hydrolysis, cytosine is converted to uracil which corresponds to thymine in its base pairing behavior. Significantly, however, 5-methylcytosine remains unmodified under these conditions. Consequently, the original DNA is *converted* in such a manner that methylcytosine, which originally could not be distinguished from cytosine by its hybridization behavior, can now be detected as the only remaining cytosine using standard, art-recognized molecular biological techniques, for example, by amplification and hybridization, or by sequencing. All of these techniques are based on differential base pairing properties, which can now be fully exploited.

The prior art, in terms of sensitivity, is defined by a method comprising enclosing the DNA to be analyzed in an agarose matrix, thereby preventing the diffusion and renaturation of the DNA (bisulfite only reacts with single-stranded DNA), and replacing all precipitation and purification steps with fast dialysis (Olek A, et al., A modified and improved method for bisulfite based cytosine methylation analysis, *Nucleic Acids Res.* 24:5064-6, 1996). It is thus possible to analyze individual cells for methylation status, illustrating the utility and sensitivity of the method. An overview of art-recognized methods for detecting 5-methylcytosine is provided by Rein, T., et al., *Nucleic Acids Res.*, 26:2255, 1998.

The bisulfite technique, barring few exceptions (e.g., Zeschnigk M, et al., *Eur J Hum Genet.* 5:94-98, 1997), is currently only used in research. In all instances, short, specific fragments of a known gene are amplified subsequent to a bisulfite treatment, and either completely sequenced (Olek & Walter, *Nat Genet.* 1997 17:275-6, 1997), subjected to one or more primer extension reactions (Gonzalzo & Jones, *Nucleic Acids Res.*, 25:2529-31, 1997; WO 95/00669; U.S. Patent No. 6,251,594) to analyze individual cytosine positions, or treated by enzymatic digestion (Xiong & Laird, *Nucleic Acids Res.*, 25:2532-4, 1997). Detection by hybridization has also been described in the art (Olek et al., WO 99/28498). Additionally, use of

the bisulfite technique for methylation detection with respect to individual genes has been described (Grigg & Clark, *Bioessays*, 16:431-6, 1994; Zeschnigk M, et al., *Hum Mol Genet.*, 6:387-95, 1997; Feil R, et al., *Nucleic Acids Res.*, 22:695-, 1994; Martin V, et al., *Gene*, 157:261-4, 1995; WO 9746705 and WO 9515373).

5 In one aspect, the present invention provides for the use of the bisulfite technique , in combination with one or more methylation assays, for determination of the methylation status of CpG dinucleotide sequences within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO:1171.

10 According to the present invention, determination of the methylation status of CpG dinucleotide sequences within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO:1171 has utility for the detection of and/or differentiation between prostate cell proliferative disorders.

Methylation Assay Procedures. Various methylation assay procedures are known in the art, and can be used in conjunction with the present invention. These assays allow for determination of the methylation state of one or a plurality of CpG dinucleotides (e.g., CpG islands) within a DNA sequence. Such assays involve, among other techniques, DNA sequencing of bisulfite-treated DNA, PCR (for sequence-specific amplification), Southern blot analysis, and use of methylation-sensitive restriction enzymes.

20 For example, genomic sequencing has been simplified for analysis of DNA methylation patterns and 5-methylcytosine distribution by using bisulfite treatment (Frommer et al., *Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). Additionally, restriction enzyme digestion of PCR products amplified from bisulfite-converted DNA is used, e.g., the method described by Sadri & Hornsby (*Nucl. Acids Res.* 24:5058-5059, 1996), or COBRA (Combined Bisulfite Restriction Analysis) (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997).

COBRA. COBRA analysis is a quantitative methylation assay useful for determining DNA methylation levels at specific gene loci in small amounts of genomic DNA (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997). Briefly, restriction enzyme digestion is used to reveal methylation-dependent sequence differences in PCR products of sodium bisulfite-treated DNA.

30 Methylation-dependent sequence differences are first introduced into the genomic DNA by standard bisulfite treatment according to the procedure described by Frommer et al. (*Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). PCR amplification of the bisulfite converted DNA is then performed using primers specific for the CpG islands of interest, followed by restriction endonuclease digestion, gel electrophoresis, and detection using specific, labeled hybridization

probes. Methylation levels in the original DNA sample are represented by the relative amounts of digested and undigested PCR product in a linearly quantitative fashion across a wide spectrum of DNA methylation levels. In addition, this technique can be reliably applied to DNA obtained from microdissected paraffin-embedded tissue samples. Typical reagents (e.g., as
5 might be found in a typical COBRA-based kit) for COBRA analysis may include, but are not limited to: PCR primers for specific gene (or bisulfite treated DNA sequence or CpG island); restriction enzyme and appropriate buffer; gene-hybridization oligo; control hybridization oligo; kinase labeling kit for oligo probe; and labelled nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery reagents or
10 kits (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

Preferably, assays such as "MethyLightTM" (a fluorescence-based real-time PCR technique) (Eads et al., *Cancer Res.* 59:2302-2306, 1999), Ms-SNuPE (Methylation-sensitive Single Nucleotide Primer Extension) reactions (Gonzalzo & Jones, *Nucleic Acids Res.* 25:2529-
15 2531, 1997), methylation-specific PCR ("MSP"; Herman et al., *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996; US Patent No. 5,786,146), and methylated CpG island amplification ("MCA"; Toyota et al., *Cancer Res.* 59:2307-12, 1999) are used alone or in combination with other of these methods.

MethyLightTM. The MethyLightTM assay is a high-throughput quantitative methylation
20 assay that utilizes fluorescence-based real-time PCR (TaqManTM) technology that requires no further manipulations after the PCR step (Eads et al., *Cancer Res.* 59:2302-2306, 1999). Briefly, the MethyLightTM process begins with a mixed sample of genomic DNA that is converted, in a sodium bisulfite reaction, to a mixed pool of methylation-dependent sequence differences according to standard procedures (the bisulfite process converts unmethylated
25 cytosine residues to uracil). Fluorescence-based PCR is then performed either in an "unbiased" (with primers that do not overlap known CpG methylation sites) PCR reaction, or in a "biased" (with PCR primers that overlap known CpG dinucleotides) reaction. Sequence discrimination can occur either at the level of the amplification process or at the level of the fluorescence detection process, or both.

30 The MethyLightTM assay may be used as a quantitative test for methylation patterns in the genomic DNA sample, wherein sequence discrimination occurs at the level of probe hybridization. In this quantitative version, the PCR reaction provides for unbiased amplification in the presence of a fluorescent probe that overlaps a particular putative methylation site. An unbiased control for the amount of input DNA is provided by a reaction in which neither the

primers, nor the probe overlies any CpG dinucleotides. Alternatively, a qualitative test for genomic methylation is achieved by probing of the biased PCR pool with either control oligonucleotides that do not “cover” known methylation sites (a fluorescence-based version of the “MSP” technique), or with oligonucleotides covering potential methylation sites.

5 The MethyLight™ process can be used with a “TaqMan®” probe in the amplification process. For example, double-stranded genomic DNA is treated with sodium bisulfite and subjected to one of two sets of PCR reactions using TaqMan® probes; e.g., with either biased primers and TaqMan® probe, or unbiased primers and TaqMan® probe. The TaqMan® probe is dual-labeled with fluorescent “reporter” and “quencher” molecules, and is designed to be
10 specific for a relatively high GC content region so that it melts out at about 10°C higher temperature in the PCR cycle than the forward or reverse primers. This allows the TaqMan® probe to remain fully hybridized during the PCR annealing/extension step. As the Taq polymerase enzymatically synthesizes a new strand during PCR, it will eventually reach the annealed TaqMan® probe. The Taq polymerase 5’ to 3’ endonuclease activity will then
15 displace the TaqMan® probe by digesting it to release the fluorescent reporter molecule for quantitative detection of its now unquenched signal using a real-time fluorescent detection system.

 Typical reagents (e.g., as might be found in a typical MethyLight™-based kit) for MethyLight™ analysis may include, but are not limited to: PCR primers for specific gene (or
20 bisulfite treated DNA sequence or CpG island); TaqMan® probes; optimized PCR buffers and deoxynucleotides; and Taq polymerase.

Ms-SNuPE. The Ms-SNuPE technique is a quantitative method for assessing methylation differences at specific CpG sites based on bisulfite treatment of DNA, followed by single-nucleotide primer extension (Gonzalzo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997).
25 Briefly, genomic DNA is reacted with sodium bisulfite to convert unmethylated cytosine to uracil while leaving 5-methylcytosine unchanged. Amplification of the desired target sequence is then performed using PCR primers specific for bisulfite-converted DNA, and the resulting product is isolated and used as a template for methylation analysis at the CpG site(s) of interest. Small amounts of DNA can be analyzed (e.g., microdissected pathology sections), and it avoids
30 utilization of restriction enzymes for determining the methylation status at CpG sites.

 Typical reagents (e.g., as might be found in a typical Ms-SNuPE-based kit) for Ms-SNuPE analysis may include, but are not limited to: PCR primers for specific gene (or bisulfite treated DNA sequence or CpG island); optimized PCR buffers and deoxynucleotides; gel extraction kit; positive control primers; Ms-SNuPE primers for specific gene; reaction buffer

(for the Ms-SNuPE reaction); and labelled nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery reagents or kit (*e.g.*, precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

5 *MSP.* MSP (methylation-specific PCR) allows for assessing the methylation status of virtually any group of CpG sites within a CpG island, independent of the use of methylation-sensitive restriction enzymes (Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996; US Patent No. 5,786,146). Briefly, DNA is modified by sodium bisulfite converting all unmethylated, but not methylated cytosines to uracil, and subsequently amplified with primers
10 specific for methylated versus unmethylated DNA. MSP requires only small quantities of DNA, is sensitive to 0.1% methylated alleles of a given CpG island locus, and can be performed on DNA extracted from paraffin-embedded samples. Typical reagents (*e.g.*, as might be found in a typical MSP-based kit) for MSP analysis may include, but are not limited to: methylated and unmethylated PCR primers for specific gene (or bisulfite treated DNA sequence or CpG island),
15 optimized PCR buffers and deoxynucleotides, and specific probes.

MCA. The MCA technique is a method that can be used to screen for altered methylation patterns in genomic DNA, and to isolate specific sequences associated with these changes (Toyota et al., *Cancer Res.* 59:2307-12, 1999). Briefly, restriction enzymes with different sensitivities to cytosine methylation in their recognition sites are used to digest genomic DNAs
20 from primary tumors, cell lines, and normal tissues prior to arbitrarily primed PCR amplification. Fragments that show differential methylation are cloned and sequenced after resolving the PCR products on high-resolution polyacrylamide gels. The cloned fragments are then used as probes for Southern analysis to confirm differential methylation of these regions. Typical reagents (*e.g.*, as might be found in a typical MCA-based kit) for MCA analysis may
25 include, but are not limited to: PCR primers for arbitrary priming Genomic DNA; PCR buffers and nucleotides, restriction enzymes and appropriate buffers; gene-hybridization oligos or probes; control hybridization oligos or probes.

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GENOMIC SEQUENCES ACCORDING TO SEQ ID NO: 1 TO SEQ ID NO: 59, SEQ ID NO: 1017 TO SEQ ID NO: 1028, SEQ ID NO: 1116 AND SEQ ID NO: 1171, AND NON-NATURALLY OCCURRING TREATED VARIANTS THEREOF ACCORDING TO SEQ ID

NOS: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175, WERE DETERMINED TO HAVE UTILITY FOR THE DETECTION, CLASSIFICATION AND/OR MONITORING OF PROSTATE CELL PROLIFERATIVE DISORDERS.

5 In one embodiment the invention provides a method for the detection of and/or differentiation between prostate cell proliferative disorders in a subject. Said method comprises the following steps

i) determining the expression levels of one or more genes or gene sequences according to Table 26 and/or regulatory regions thereof

10 ii) determining the presence or absence of a prostate cell proliferative disorders according to said level of expression.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1, 15 PROTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027.

20 Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or 25 neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from Table 26 are analysed.

30 It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting GSTP1, PROTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO:

1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

5 Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

10 Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide
15 sequence.

 Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at
20 least one CpG, TpG or CpA dinucleotide sequence.

Said expression level may be determined by any means standard in the art including but not limited to methylation analysis, loss of heterozygosity (hereinafter also referred to as LOH), RNA expression levels and protein expression levels.

 Said use of the genes and/or sequences may be enabled by means of any analysis of the
25 expression of the gene, by means of mRNA expression analysis or protein expression analysis. However, in the most preferred embodiment of the invention, the detection of and/or differentiation between prostate cell proliferative disorders is enabled by means of analysis of the methylation status of said genes or genomic sequences and their promoter or regulatory elements. Methods for the methylation analysis of genes are described herein.

30 In one embodiment the method discloses the use of one or more genes or genomic sequences selected from the group consisting the genes according to Table 26 as markers for the detection of and/or differentiation between prostate cell proliferative disorders.

 Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes

and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from Table 26 are analysed.

It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according

to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Said use of the genes and/or sequences may be enabled by means of any analysis of the expression of the gene, by means of mRNA expression analysis or protein expression analysis.

However, in the most preferred embodiment of the invention, the detection of and/or differentiation between prostate cell proliferative disorders is enabled by means of analysis of the methylation status of said genes or genomic sequences and their promoter or regulatory elements. Methods for the methylation analysis of genes are described herein.

Aberrant levels of mRNA expression of the genes, genomic sequences or genes regulated by genomic sequences according to Table 26 are associated with presence of prostate cell proliferative disorders. Accordingly, increased or decreased levels of expression of said genes or sequences are associable with factors associated with the presence of prostate cell proliferative disorders; and are indicative of sub-types thereof.

To detect the presence of mRNA encoding a gene or genomic sequence in a detection of and/or differentiation between prostate cell proliferative disorders, a sample is obtained from a patient. Preferably, the source of the DNA sample is selected from the group consisting of cells or cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof. Preferably, the source is biopsies, bodily fluids, ejaculate, urine, or blood. The sample may be treated to extract the nucleic acids contained therein. The resulting nucleic acid from the sample is subjected to gel electrophoresis or other separation techniques. Detection involves contacting the nucleic acids and in particular the mRNA of the sample with a DNA sequence serving as a probe to form hybrid duplexes. The stringency of hybridisation is determined by a number of factors during hybridisation and during the washing procedure, including temperature, ionic strength, length of time and concentration of formamide. These factors are outlined in, for example, Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2d ed., 1989). Detection of the resulting duplex is usually accomplished by the use of labelled probes. Alternatively, the probe may be unlabeled, but may be detectable by specific binding with a ligand which is labelled, either directly or indirectly. Suitable labels and methods for labelling probes and ligands are known in the art, and include, for example,

radioactive labels which may be incorporated by known methods (e.g., nick translation or kinasing), biotin, fluorescent groups, chemiluminescent groups (e.g., dioxetanes, particularly triggered dioxetanes), enzymes, antibodies, and the like.

In order to increase the sensitivity of the detection in a sample of mRNA transcribed from the gene or genomic sequence, the technique of reverse transcription/polymerisation chain reaction can be used to amplify cDNA transcribed from the mRNA. The method of reverse transcription /PCR is well known in the art (for example, see Watson and Fleming, *supra*).

The reverse transcription /PCR method can be performed as follows. Total cellular RNA is isolated by, for example, the standard guanidium isothiocyanate method and the total RNA is reverse transcribed. The reverse transcription method involves synthesis of DNA on a template of RNA using a reverse transcriptase enzyme and a 3' end primer. Typically, the primer contains an oligo(dT) sequence. The cDNA thus produced is then amplified using the PCR method and EYA4 specific primers. (Belyavsky et al, Nucl Acid Res 17:2919-2932, 1989; Krug and Berger, *Methods in Enzymology*, Academic Press, N.Y., Vol.152, pp. 316-325, 1987 which are incorporated by reference)

Aberrant levels of polypeptide expression of the polypeptides encoded by the genes, genomic sequences or genes regulated by genomic sequences of the group consisting all genes and genomic sequences of genomic regions listed in Table 26 are associated with the detection of and/or differentiation between prostate cell proliferative disorders. Accordingly over or under expression of said polypeptides are associable with the presence of prostate carcinoma, prostate neoplasms and other prostate cell proliferative disorders.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1, PROTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate

cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from Table 26 are analysed.

It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEOBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Any method known in the art for detecting proteins can be used. Such methods include, but are not limited to immunodiffusion, immunoelectrophoresis, immunochemical methods, binder-ligand assays, immunohistochemical techniques, agglutination and complement assays.

(for example see Basic and Clinical Immunology, Sites and Terr, eds., Appleton & Lange, Norwalk, Conn. pp 217-262, 1991 which is incorporated by reference). Preferred are binder-ligand immunoassay methods including reacting antibodies with an epitope or epitopes and competitively displacing a labelled protein or derivative thereof.

5 Certain embodiments of the present invention comprise the use of antibodies specific to the polypeptide encoded by the genes or genomic sequences of the group consisting all genes and genomic sequences of genomic regions listed in Table 26 .

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes
 10 and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED
 15 MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate
 20 cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and
 25 one or more genes and/or sequences selected from Table 26 are analysed.

It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028,
 30 LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Such antibodies may be useful for detection applications, by comparing a patient's levels of prostate marker expression to expression of the same markers in healthy individuals. In certain embodiments production of monoclonal or polyclonal antibodies can be induced by the use of the coded polypeptide as antigene. Such antibodies may in turn be used to detect expressed proteins as markers for human disease states. The levels of such proteins present in the peripheral blood or tissue sample of a patient may be quantified by conventional methods. Antibody-protein binding may be detected and quantified by a variety of means known in the art, such as labelling with fluorescent or radioactive ligands. The invention further comprises kits for performing the above-mentioned procedures, wherein such kits contain antibodies specific for the investigated polypeptides.

Numerous competitive and non-competitive protein binding immunoassays are well known in the art. Antibodies employed in such assays may be unlabeled, for example as used in agglutination tests, or labelled for use a wide variety of assay methods. Labels that can be used include radionuclides, enzymes, fluorescers, chemiluminescers, enzyme substrates or co-factors, enzyme inhibitors, particles, dyes and the like for use in radioimmunoassay (RIA), enzyme immunoassays, e.g., enzyme-linked immunosorbent assay (ELISA), fluorescent immunoassays and the like. Polyclonal or monoclonal antibodies or epitopes thereof can be made for use in immunoassays by any of a number of methods known in the art. One approach for preparing

antibodies to a protein is the selection and preparation of an amino acid sequence of all or part of the protein, chemically synthesising the sequence and injecting it into an appropriate animal, usually a rabbit or a mouse (Milstein and Kohler Nature 256:495-497, 1975; Gutfre and Milstein, Methods in Enzymology: Immunochemical Techniques 73:1-46, Langone and Banatis eds., Academic Press, 1981 which are incorporated by reference). Methods for preparation of the polypeptides or epitopes thereof include, but are not limited to chemical synthesis, recombinant DNA techniques or isolation from biological samples.

In a particularly preferred embodiment the expression level of the genes and/or genomic sequences according to Table 26 is determined by analysis of the level of methylation of said genes, genomic sequences and/or regulatory regions thereof..

Said analysis comprises the following steps:

i) contacting genomic DNA obtained from the subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides within at least one target region of the genomic DNA, wherein said contiguous nucleotides comprise at least one CpG dinucleotide sequence,

ii) determining the presence or absence of a prostate cell proliferative disorders and/or a classification thereof according to the methylation status of said target regions analysed in i).

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1, PROTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly

preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from Table 26 are analysed.

It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE
5 H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

10 Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous
15 nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or
20 more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under
25 stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

In the first step of said methylation analysis the genomic DNA to be analysed is isolated. Genomic DNA may be isolated by any means standard in the art, including the use of
30 commercially available kits. Briefly, wherein the DNA of interest is encapsulated in by a cellular membrane the biological sample must be disrupted and lysed by enzymatic, chemical or mechanical means. The DNA solution may then be cleared of proteins and other contaminants e.g. by digestion with proteinase K. The genomic DNA is then recovered from the solution. This may be carried out by means of a variety of methods including salting out, organic

extraction or binding of the DNA to a solid phase support. The choice of method will be affected by several factors including time, expense and required quantity of DNA.

Preferably, the source of the DNA sample is selected from the group consisting of cells or cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof. Preferably, the source is biopsies, bodily fluids, ejaculate, urine, or blood.

The genomic DNA sample is then treated in such a manner that cytosine bases which are unmethylated at the 5'-position are converted to uracil, thymine, or another base which is dissimilar to cytosine in terms of hybridization behavior. This will be understood as 'treatment' herein.

The above described treatment of genomic DNA is preferably carried out with bisulfite (hydrogen sulfite, disulfite) and subsequent alkaline hydrolysis which results in a conversion of non-methylated cytosine nucleobases to uracil or to another base which is dissimilar to cytosine in terms of base pairing behavior.

The treated DNA is then analysed in order to determine the methylation state of one or more target gene sequences (prior to the treatment) associated with the presence of prostate cell proliferative disorders and/or indicative of the presence of sub-types thereof. It is particularly preferred that the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of at least one gene or genomic sequence selected from the group consisting the genes and genomic sequences as listed in Table 26. It is further preferred that the sequences of said genes in Table 26 as described in the accompanying sequence listing are analysed.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to a sequence comprising at least 16 contiguous nucleotides of the sequences selected from the group consisting of SEQ ID NO: 1023, SEQ ID NO: 57, SEQ ID NO: 20, SEQ ID NO: 36, SEQ ID NO: 1171, SEQ ID NO: 51, SEQ ID NO: 31, SEQ ID NO: 24, SEQ ID NO: 11, SEQ ID NO: 1028, SEQ ID NO: 4, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, SEQ ID NO: 18, SEQ ID NO: 1019 and SEQ ID NO: 1027. Accordingly it is preferred that subsequent to treatment said sequences are converted to the corresponding converted or non-converted dinucleotide sequence is selected from the group consisting of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173,

160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050, and contiguous regions thereof according to Table 26.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to a sequence comprising at least 16 contiguous nucleotides of the sequences selected from the group consisting of SEQ ID NO: 57 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is particularly preferred that SEQ ID NO: 57 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or neoplasms and/or differentiation thereof from benign prostate hyperplasia it is particularly preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from Table 26 are analysed.

It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according

to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

The method of analysis may be selected from those known in the art, including those listed herein. Particularly preferred are MethyLight, MSP and the use of blocking oligonucleotides as will be described herein. It is further preferred that any oligonucleotides used in such analysis (including primers, blocking oligonucleotides and detection probes) should be reverse complementary, identical, or hybridize under stringent or highly stringent conditions to an at least 16-base-pair long segment of the base sequences of one or more of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 and sequences complementary thereto. It is further preferred that any oligonucleotides used in such analysis (including primers, blocking oligonucleotides and detection probes) should be reverse complementary, identical, or hybridize under stringent or highly stringent conditions to an at least 16-base-pair long segment of the base sequences of one or more of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 and sequences complementary thereto.

Aberrant methylation, more preferably hypermethylation of one or more genes or genomic sequences taken from those listed in Table 26 are associated with the presence of prostate cell proliferative disorders. Analysis of one or a plurality of the sequences enables the detection of and/or differentiation between prostate cell proliferative disorders.

In one embodiment the method discloses the use of one or more genes or genomic sequences selected from the group consisting the genes according to Table 26 as markers for the detection of and/or differentiation between prostate cell proliferative disorders.

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ

ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027

Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from Table 26 are analysed.

It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting GSTP1, PROSTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEOBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under

stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

5 The present invention may also be described in certain embodiments as a kit for use in the detection of and/or differentiation between a prostate cell proliferative disorder state through testing of a biological sample. A representative kit may comprise one or more nucleic acid segments that selectively hybridise to the mRNA and a container for each of the one or more nucleic acid segments. In certain embodiments the nucleic acid segments may be combined in a single tube. In further embodiments, the nucleic acid segments may also include a pair of
10 primers for amplifying the target mRNA. Such kits may also include any buffers, solutions, solvents, enzymes, nucleotides, or other components for hybridisation, amplification or detection reactions. Preferred kit components include reagents for reverse transcription-PCR, in situ hybridisation, Northern analysis and/or RPA

Particular embodiments of the present invention provide a novel application of the
15 analysis of methylation levels and/or patterns within said sequences that enables the early detection and thereby improved treatment of prostate cell proliferative disorders, furthermore said method enables the differentiation of benign conditions from conditions such as prostate carcinoma and neoplasms which may be potentially malignant and have much more serious health consequences for the patient. Treatment of prostate cell proliferative disorders is
20 improved by early detection, and the disclosed method thereby enables the physician and patient to make better and more informed treatment decisions.

FURTHER IMPROVEMENTS

25 The present invention provides novel uses for genomic sequences selected from the group consisting of SEQ ID NO: 1 TO SEQ ID NO: 59, SEQ ID NO: 1017 TO SEQ ID NO: 1028, SEQ ID NO: 1116 AND SEQ ID NO:1171 . Additional embodiments provide modified variants of SEQ ID NO: 1 TO SEQ ID NO: 59, SEQ ID NO: 1017 TO SEQ ID NO: 1028, SEQ ID NO: 1116 AND SEQ ID NO:1171 , as well as oligonucleotides and/or PNA-oligomers for
30 analysis of cytosine methylation patterns within the group consisting SEQ ID NO: 1 TO SEQ ID NO: 59, SEQ ID NO: 1017 TO SEQ ID NO: 1028, SEQ ID NO: 1116 AND SEQ ID NO:1171 .

An objective of the invention comprises analysis of the methylation state of one or more CpG dinucleotides within at least one of the genomic sequences selected from the group

consisting of SEQ ID NO: 1 TO SEQ ID NO: 59, SEQ ID NO: 1017 TO SEQ ID NO: 1028, SEQ ID NO: 1116 AND SEQ ID NO: 1171 and sequences complementary thereto.

The disclosed invention provides treated nucleic acids, derived from genomic SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization. The genomic sequences in question may comprise one, or more, consecutive or random methylated CpG positions. Said treatment preferably comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof. In a preferred embodiment of the invention, the objective comprises analysis of a non-naturally occurring modified nucleic acid comprising a sequence of at least 16 contiguous nucleotide bases in length of a sequence selected from the group consisting of SEQ ID NOS: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175, wherein said sequence comprises at least one CpG, TpA or CpA dinucleotide and sequences complementary thereto. In a further preferred embodiment of the invention, the objective comprises analysis of a non-naturally occurring modified nucleic acid comprising a sequence of at least 16 contiguous nucleotide bases in length of a sequence selected from the group consisting of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 wherein said sequence comprises at least one CpG, TpA or CpA dinucleotide and sequences complementary thereto. The sequences of SEQ ID NO: 60- 295, 1029-1076, 1117 – 1120, 1171 – 1175 provide non-naturally occurring modified versions of the nucleic acid according to SEQ ID NO: 1 TO SEQ ID NO: 59, SEQ ID NO: 1017 TO SEQ ID NO: 1028, SEQ ID NO: 1116 AND SEQ ID NO: 1171, wherein the modification of each genomic sequence results in the synthesis of a nucleic acid having a sequence that is unique and distinct from said genomic sequence as follows. For each sense strand genomic DNA, *e.g.*, SEQ ID NO: 1, four converted versions are disclosed. A first version wherein "C" is converted to "T," but "CpG" remains "CpG" (*i.e.*, corresponds to case where, for the genomic sequence, all "C" residues of CpG dinucleotide sequences are methylated and are thus not converted); a second version discloses the complement of the disclosed genomic DNA sequence (*i.e.* *antisense* strand), wherein "C" is converted to "T," but "CpG" remains "CpG" (*i.e.*, corresponds to case where, for all "C" residues of CpG dinucleotide sequences are methylated and are thus not converted).

In an alternative preferred embodiment, such analysis comprises the use of an oligonucleotide or oligomer for detecting the cytosine methylation state within genomic or

treated (non-naturally occurring modified) DNA, according to SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116, SEQ ID NO: 1171, SEQ ID NO: 60- 295, 1029-1076, 1117 – 1120, 1171 – 1175. In a preferred embodiment, such analysis comprises the use of an oligonucleotide or oligomer for detecting the cytosine methylation state within genomic or treated (chemically modified) DNA, according to SEQ ID NOS: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050.

Said oligonucleotide or oligomer each comprising a nucleic acid sequence having a length of at least nine (9) nucleotides which hybridizes, under moderately stringent or stringent conditions (as defined herein above), to a treated nucleic acid sequence according to SEQ ID NO: 60- 295, 1029-1076, 1117 – 1120, 1171 – 1175 and/or sequences complementary thereto, or to a genomic sequence according to SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 and/or sequences complementary thereto.

Particularly preferred is an oligonucleotide or oligomer comprising a nucleic acid sequence having a length of at least nine (9) nucleotides which hybridizes, under moderately stringent or stringent conditions (as defined herein above), to a treated nucleic acid sequence according to SEQ ID NOS: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 and/or sequences complementary thereto.

Thus, the present invention includes nucleic acid molecules (*e.g.*, oligonucleotides and peptide nucleic acid (PNA) molecules (PNA-oligomers)) that hybridize under moderately stringent and/or stringent hybridization conditions to all or a portion of the sequences SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116, SEQ ID NO: 1171, SEQ ID NOS: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 , or to the complements thereof. The hybridizing portion of the hybridizing nucleic acids is typically at least 9, 15, 20, 25, 30 or 35 nucleotides in length. However, longer molecules have inventive utility, and are thus within the scope of the present invention.

Preferably, the hybridizing portion of the inventive hybridizing nucleic acids is at least 95%, or at least 98%, or 100% identical to the sequence, or to a portion thereof of SEQ ID NOS: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 or to the complements thereof.

Hybridizing nucleic acids of the type described herein can be used, for example, as a primer (*e.g.*, a PCR primer), or a diagnostic and/or classification probe or primer. Preferably, hybridization of the oligonucleotide probe to a nucleic acid sample is performed under stringent

conditions and the probe is 100% identical to the target sequence. Nucleic acid duplex or hybrid stability is expressed as the melting temperature or T_m , which is the temperature at which a probe dissociates from a target DNA. This melting temperature is used to define the required stringency conditions.

5 For target sequences that are related and substantially identical to the corresponding sequence of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 (such as allelic variants and SNPs), rather than identical, it is useful to first establish the lowest temperature at which only homologous hybridization occurs with a particular concentration of salt (*e.g.*, SSC or SSPE). Then, assuming that 1% mismatching results in a 1°C decrease in the T_m , the temperature of the final wash in the hybridization reaction is reduced accordingly (for example, if sequences having > 95% identity with the probe are sought, the final wash temperature is decreased by 5°C). In practice, the change in T_m can be between 0.5°C and 1.5°C per 1% mismatch.

15 Examples of inventive oligonucleotides of length X (in nucleotides), as indicated by polynucleotide positions with reference to, *e.g.*, SEQ ID NO:1, include those corresponding to sets (sense and antisense sets) of consecutively overlapping oligonucleotides of length X, where the oligonucleotides within each consecutively overlapping set (corresponding to a given X value) are defined as the finite set of Z oligonucleotides from nucleotide positions: n to (n + (X-1));

20 where $n=1, 2, 3, \dots, (Y-(X-1))$;
 where Y equals the length (nucleotides or base pairs) of SEQ ID NO: 1 (2299);
 where X equals the common length (in nucleotides) of each oligonucleotide in the set (*e.g.*, X=20 for a set of consecutively overlapping 20-mers); and
 where the number (Z) of consecutively overlapping oligomers of length X for a given
 25 SEQ ID NO of length Y is equal to $Y-(X-1)$. For example $Z=2299-19=2280$ for either sense or antisense sets of SEQ ID NO:1, where X=20.

Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

30 Examples of inventive 20-mer oligonucleotides include the following set of 2280 oligomers (and the antisense set complementary thereto), indicated by polynucleotide positions with reference to SEQ ID NO:1:
 1-20, 2-21, 3-22, 4-23, 5-24,2280 -2299.

Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

Likewise, examples of inventive 25-mer oligonucleotides include the following set of 2,256 oligomers (and the antisense set complementary thereto), indicated by polynucleotide positions with reference to SEQ ID NO:1:

1-25, 2-26, 3-27, 4-28, 5-29,2280 -2299.

5 Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

The present invention encompasses, for *each* of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116, SEQ ID NO:1171, SEQ ID NOs: 60-295, 1029-1076, 1117 – 1120, 1172 – 1175 (sense and antisense), multiple consecutively
10 overlapping sets of oligonucleotides or modified oligonucleotides of length X, where, *e.g.*, X= 9, 10, 17, 20, 22, 23, 25, 27, 30 or 35 nucleotides.

The oligonucleotides or oligomers according to the present invention constitute effective tools useful to ascertain genetic and epigenetic parameters of the genomic sequence corresponding to SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028,
15 SEQ ID NO: 1116 and SEQ ID NO:1171 . Preferably, said oligomers comprise at least one CpG, TpG or CpA dinucleotide.

Particularly preferred oligonucleotides or oligomers according to the present invention are those in which the cytosine of the CpG dinucleotide (or of the corresponding converted TpG or CpA dinucleotide) sequences is within the middle third of the oligonucleotide; that is, where
20 the oligonucleotide is, for example, 13 bases in length, the CpG, TpG or CpA dinucleotide is positioned within the fifth to ninth nucleotide from the 5'-end.

The oligonucleotides of the invention can also be modified by chemically linking the oligonucleotide to one or more moieties or conjugates to enhance the activity, stability or detection of the oligonucleotide. Such moieties or conjugates include chromophores,
25 fluorophors, lipids such as cholesterol, cholic acid, thioether, aliphatic chains, phospholipids, polyamines, polyethylene glycol (PEG), palmityl moieties, and others as disclosed in, for example, United States Patent Numbers 5,514,758, 5,565,552, 5,567,810, 5,574,142, 5,585,481, 5,587,371, 5,597,696 and 5,958,773. The probes may also exist in the form of a PNA (peptide nucleic acid) which has particularly preferred pairing properties. Thus, the oligonucleotide
30 may include other appended groups such as peptides, and may include hybridization-triggered cleavage agents (Krol et al., *BioTechniques* 6:958-976, 1988) or intercalating agents (Zon, *Pharm. Res.* 5:539-549, 1988). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a chromophore, fluorophor, peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The oligonucleotide may also comprise at least one art-recognized modified sugar and/or base moiety, or may comprise a modified backbone or non-natural internucleoside linkage.

The oligonucleotides or oligomers according to particular embodiments of the present invention are typically used in 'sets,' which contain at least one oligomer for analysis of each of the CpG dinucleotides of genomic sequences SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 and sequences complementary thereto, or to the corresponding CpG, TpG or CpA dinucleotide within a sequence of the treated nucleic acids according to SEQ ID NO: 60- 295, 1029-1076, 1117 – 1120, 1171 – 1175 1017 to SEQ ID NO: 1028 and sequences complementary thereto. However, it is anticipated that for economic or other factors it may be preferable to analyze a limited selection of the CpG dinucleotides within said sequences, and the content of the set of oligonucleotides is altered accordingly.

Therefore, in particular embodiments, the present invention provides a set of at least two (2) (oligonucleotides and/or PNA-oligomers) useful for detecting the cytosine methylation state in treated genomic DNA (SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175), or in genomic DNA (SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 and sequences complementary thereto). These probes enable diagnosis and/or classification of genetic and epigenetic parameters of prostate cell proliferative disorders. The set of oligomers may also be used for detecting single nucleotide polymorphisms (SNPs) in treated genomic DNA (SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175), or in genomic DNA (SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 and sequences complementary thereto).

Particularly preferred is a set of at least two (2) (oligonucleotides and/or PNA-oligomers) useful for detecting the cytosine methylation state in treated genomic DNA according to SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050.

In preferred embodiments, at least one, and more preferably all members of a set of oligonucleotides is bound to a solid phase.

In further embodiments, the present invention provides a set of at least two (2) oligonucleotides that are used as 'primer' oligonucleotides for amplifying DNA sequences of one of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116, SEQ ID NO: 1171, SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 and sequences complementary thereto, or segments thereof.

Particularly preferred is a set of at least two (2) oligonucleotides that are used as 'primer' oligonucleotides for amplifying DNA sequences of one of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050.

5 It is anticipated that the oligonucleotides may constitute all or part of an "array" or "DNA chip" (*i.e.*, an arrangement of different oligonucleotides and/or PNA-oligomers bound to a solid phase). Such an array of different oligonucleotide- and/or PNA-oligomer sequences can be characterized, for example, in that it is arranged on the solid phase in the form of a rectangular or hexagonal lattice. The solid-phase surface may be composed of silicon, glass, polystyrene,
10 aluminum, steel, iron, copper, nickel, silver, or gold. Nitrocellulose as well as plastics such as nylon, which can exist in the form of pellets or also as resin matrices, may also be used. An overview of the Prior Art in oligomer array manufacturing can be gathered from a special edition of Nature Genetics (*Nature Genetics Supplement*, Volume 21, January 1999, and from the literature cited therein). Fluorescently labeled probes are often used for the scanning of
15 immobilized DNA arrays. The simple attachment of Cy3 and Cy5 dyes to the 5'-OH of the specific probe are particularly suitable for fluorescence labels. The detection of the fluorescence of the hybridized probes may be carried out, for example, via a confocal microscope. Cy3 and Cy5 dyes, besides many others, are commercially available.

It is also anticipated that the oligonucleotides, or particular sequences thereof, may
20 constitute all or part of a "virtual array" wherein the oligonucleotides, or particular sequences thereof, are used, for example, as 'specifiers' as part of, or in combination with a diverse population of unique labeled probes to analyze a complex mixture of analytes. Such a method, for example is described in US 2003/0013091 (United States serial number 09/898,743, published 16 January 2003). In such methods, enough labels are generated so that each nucleic
25 acid in the complex mixture (*i.e.*, each analyte) can be uniquely bound by a unique label and thus detected (each label is directly counted, resulting in a digital read-out of each molecular species in the mixture).

It is particularly preferred that the oligomers according to the invention are utilised for at least one of: detection of; screening of populations for; differentiation between; monitoring of;
30 and detection and monitoring of prostate cell proliferative disorders. This is enabled by use of said sets for the detection of and/or differentiation between prostate cell proliferative disorders in a biological sample isolated from a patient. Particularly preferred are those sets of oligomer that comprise at least two oligonucleotides selected from one of the following sets of oligonucleotides.

In one embodiment of the method, this is achieved by analysis of the methylation status of at least one target sequence comprising, or hybridizing under stringent conditions to at least 16 contiguous nucleotides of a gene or sequence selected from the group consisting the genes and sequences according to Table 26 and complements thereof.

5 Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is preferred that said genes and/or sequences are selected from the group consisting of SEQ ID NO: 1023, GSTP1, PROTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ
10 ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027.

 Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is also preferred that said
15 genes and/or sequences are Gstp1 and one or more sequences selected from the group consisting of SEQ ID NO: 1017 to SEQ ID NO: 1028. Wherein the method is for the diagnosis of prostate cell proliferative disorders, (most preferably prostate cancer, prostate carcinoma and/or neoplasms) it is particularly preferred that Gstp1 and SEQ ID NO: 1023 are analysed.

 Wherein the method is for the diagnosis of prostate cancer, prostate carcinoma and/or
20 neoplasms and or differentiation thereof from benign prostate hyperplasia it is particularly preferred that SEQ ID NO: 1023 is analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from Table 26 are analysed. It is also preferred that SEQ ID NO: 1023 and one or more genes and/or sequences selected from the group consisting
25 GSTP1, PROTAGLANDIN E2 RECEPTOR, HISTONE H4, RASSF1A, PR-DOMAIN ZINC FINGER PROTEIN 16, LIM DOMAIN KINASE 1, ORPHAN NUCLEAR RECEPTOR NR5A2, SEQ ID NO: 11, SEQ ID NO: 1028, LIM/HOMEBOX PROTEIN LHX9, SEQ ID NO: 1116, SEQ ID NO: 1025, SEQ ID NO: 1020, LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN, SEQ ID NO: 1019 and SEQ ID NO: 1027 are analysed.

30 Particularly preferred are the combinations of genes described in Tables 22 and 23, in particular the analysis of SEQ ID NO: 1023 and GSTP1.

 Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous

nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

The present invention further provides a method for ascertaining genetic and/or epigenetic parameters of the genomic sequences according to SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO:1171 within a subject by analyzing cytosine methylation and single nucleotide polymorphisms. Said method comprising contacting a nucleic acid comprising one or more of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO:1171 in a biological sample obtained from said subject with at least one reagent or a series of reagents, wherein said reagent or series of reagents, distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid.

Preferably, said method comprises the following steps: In the *first step*, a sample of the tissue to be analysed is obtained. Preferably, the source of the DNA sample is selected from the group consisting of cells or cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof. Preferably, the source is biopsies, bodily fluids, ejaculate, urine, or blood.

The genomic DNA is then isolated from the sample. Genomic DNA may be isolated by any means standard in the art, including the use of commercially available kits. Briefly, wherein the DNA of interest is encapsulated in by a cellular membrane the biological sample must be disrupted and lysed by enzymatic, chemical or mechanical means. The DNA solution may then be cleared of proteins and other contaminants e.g. by digestion with proteinase K. The genomic DNA is then recovered from the solution. This may be carried out by means of a variety of methods including salting out, organic extraction or binding of the DNA to a solid phase

support. The choice of method will be affected by several factors including time, expense and required quantity of DNA.

Once the nucleic acids have been extracted, the genomic double stranded DNA is used in the analysis.

5 In the *second step* of the method, the genomic DNA sample is treated in such a manner that cytosine bases which are unmethylated at the 5'-position are converted to uracil, thymine, or another base which is dissimilar to cytosine in terms of hybridization behavior. This will be understood as 'pretreatment' or 'treatment' herein.

10 The above-described treatment of genomic DNA is preferably carried out with bisulfite (hydrogen sulfite, disulfite) and subsequent alkaline hydrolysis which results in a conversion of non-methylated cytosine nucleobases to uracil or to another base which is dissimilar to cytosine in terms of base pairing behavior.

15 In the *third step* of the method, fragments of the treated DNA are amplified, using sets of primer oligonucleotides according to the present invention, and an amplification enzyme. The amplification of several DNA segments can be carried out simultaneously in one and the same reaction vessel. Typically, the amplification is carried out using a polymerase chain reaction (PCR). The set of primer oligonucleotides includes at least two oligonucleotides whose sequences are each reverse complementary, identical, or hybridize under stringent or highly stringent conditions to an at least 16-base-pair long segment of the base sequences of one of
20 SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 and sequences complementary thereto.

Particularly preferred is a set of primer oligonucleotides includes at least two oligonucleotides whose sequences are each reverse complementary, identical, or hybridize under stringent or highly stringent conditions to an at least 16-base-pair long segment of the base
25 sequences of one of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 and sequences complementary thereto.

In an alternate embodiment of the method, the methylation status of preselected CpG positions within the nucleic acid sequences comprising one or more of SEQ ID NO: 1 to SEQ ID
30 NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171 may be detected by use of methylation-specific primer oligonucleotides. This technique (MSP) has been described in United States Patent No. 6,265,171 to Herman. The use of methylation status specific primers for the amplification of bisulfite treated DNA allows the differentiation between methylated and unmethylated nucleic acids. MSP primers pairs contain at least one

primer which hybridizes to a bisulfite treated CpG dinucleotide. Therefore, the sequence of said primers comprises at least one CpG dinucleotide. MSP primers specific for non-methylated DNA contain a "T" at the position of the C position in the CpG. Preferably, therefore, the base sequence of said primers is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

Preferably, the base sequence of said primers is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

A further preferred embodiment of the method comprises the use of *blocker* oligonucleotides. The use of such blocker oligonucleotides has been described by Yu et al., *BioTechniques* 23:714-720, 1997. Blocking probe oligonucleotides are hybridized to the bisulfite treated nucleic acid concurrently with the PCR primers. PCR amplification of the nucleic acid is terminated at the 5' position of the blocking probe, such that amplification of a nucleic acid is suppressed where the complementary sequence to the blocking probe is present. The probes may be designed to hybridize to the bisulfite treated nucleic acid in a methylation status specific manner. For example, for detection of methylated nucleic acids within a population of unmethylated nucleic acids, suppression of the amplification of nucleic acids which are unmethylated at the position in question would be carried out by the use of blocking probes comprising a 'CpA' or 'TpA' at the position in question, as opposed to a 'CpG' if the suppression of amplification of methylated nucleic acids is desired.

For PCR methods using blocker oligonucleotides, efficient disruption of polymerase-mediated amplification requires that blocker oligonucleotides not be elongated by the polymerase. Preferably, this is achieved through the use of blockers that are 3'-deoxyoligonucleotides, or oligonucleotides derivitized at the 3' position with other than a "free" hydroxyl group. For example, 3'-O-acetyl oligonucleotides are representative of a preferred class of blocker molecule.

Additionally, polymerase-mediated decomposition of the blocker oligonucleotides should be precluded. Preferably, such preclusion comprises either use of a polymerase lacking 5'-3' exonuclease activity, or use of modified blocker oligonucleotides having, for example,

thioate bridges at the 5'-termini thereof that render the blocker molecule nuclease-resistant. Particular applications may not require such 5' modifications of the blocker. For example, if the blocker- and primer-binding sites overlap, thereby precluding binding of the primer (*e.g.*, with excess blocker), degradation of the blocker oligonucleotide will be substantially precluded. This is because the polymerase will not extend the primer toward, and through (in the 5'-3' direction) the blocker—a process that normally results in degradation of the hybridized blocker oligonucleotide.

A particularly preferred blocker/PCR embodiment, for purposes of the present invention and as implemented herein, comprises the use of peptide nucleic acid (PNA) oligomers as blocking oligonucleotides. Such PNA blocker oligomers are ideally suited, because they are neither decomposed nor extended by the polymerase.

Preferably, therefore, the base sequence of said *blocking oligonucleotides* is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 and sequences complementary thereto, wherein the base sequence of said oligonucleotides comprises at least one CpG, TpG or CpA dinucleotide.

It is further preferred that the base sequence of said *blocking oligonucleotides* is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 and sequences complementary thereto, wherein the base sequence of said oligonucleotides comprises at least one CpG, TpG or CpA dinucleotide.

The fragments obtained by means of the amplification can carry a directly or indirectly detectable label. Preferred are labels in the form of fluorescence labels, radionuclides, or detachable molecule fragments having a typical mass which can be detected in a mass spectrometer. Where said labels are mass labels, it is preferred that the labeled amplicates have a single positive or negative net charge, allowing for better detectability in the mass spectrometer. The detection may be carried out and visualized by means of, *e.g.*, matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI).

Matrix Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-TOF) is a very efficient development for the analysis of biomolecules (Karas & Hillenkamp, *Anal Chem.*, 60:2299-301, 1988). An analyte is embedded in a light-absorbing matrix. The matrix is evaporated by a short laser pulse thus transporting the analyte molecule into the vapour phase in

an unfragmented manner. The analyte is ionized by collisions with matrix molecules. An applied voltage accelerates the ions into a field-free flight tube. Due to their different masses, the ions are accelerated at different rates. Smaller ions reach the detector sooner than bigger ones. MALDI-TOF spectrometry is well suited to the analysis of peptides and proteins. The analysis of nucleic acids is somewhat more difficult (Gut & Beck, *Current Innovations and Future Trends*, 1:147-57, 1995). The sensitivity with respect to nucleic acid analysis is approximately 100-times less than for peptides, and decreases disproportionately with increasing fragment size. Moreover, for nucleic acids having a multiply negatively charged backbone, the ionization process via the matrix is considerably less efficient. In MALDI-TOF spectrometry, the selection of the matrix plays an eminently important role. For desorption of peptides, several very efficient matrixes have been found which produce a very fine crystallisation. There are now several responsive matrixes for DNA, however, the difference in sensitivity between peptides and nucleic acids has not been reduced. This difference in sensitivity can be reduced, however, by chemically modifying the DNA in such a manner that it becomes more similar to a peptide. For example, phosphorothioate nucleic acids, in which the usual phosphates of the backbone are substituted with thiophosphates, can be converted into a charge-neutral DNA using simple alkylation chemistry (Gut & Beck, *Nucleic Acids Res.* 23: 1367-73, 1995). The coupling of a charge tag to this modified DNA results in an increase in MALDI-TOF sensitivity to the same level as that found for peptides. A further advantage of charge tagging is the increased stability of the analysis against impurities, which makes the detection of unmodified substrates considerably more difficult.

In the *fourth step* of the method, the amplicates obtained during the third step of the method are analysed in order to ascertain the methylation status of the CpG dinucleotides prior to the treatment.

In embodiments where the amplicates were obtained by means of MSP amplification, the presence or absence of an amplicate is in itself indicative of the methylation state of the CpG positions covered by the primer, according to the base sequences of said primer.

Amplicates obtained by means of both standard and methylation specific PCR may be further analyzed by means of hybridization-based methods such as, but not limited to, array technology and probe based technologies as well as by means of techniques such as sequencing and template directed extension.

In one embodiment of the method, the amplicates synthesised in *step three* are subsequently hybridized to an array or a set of oligonucleotides and/or PNA probes. In this context, the hybridization takes place in the following manner: the set of probes used during the

hybridization is preferably composed of at least 2 oligonucleotides or PNA-oligomers; in the process, the amplicates serve as probes which hybridize to oligonucleotides previously bonded to a solid phase; the non-hybridized fragments are subsequently removed; said oligonucleotides contain at least one base sequence having a length of at least 9 nucleotides which is reverse complementary or identical to a segment of the base sequences specified in the present Sequence Listing; and the segment comprises at least one CpG, TpG or CpA dinucleotide.

In a preferred embodiment, said dinucleotide is present in the central third of the oligomer. For example, wherein the oligomer comprises one CpG dinucleotide, said dinucleotide is preferably the fifth to ninth nucleotide from the 5'-end of a 13-mer. One oligonucleotide exists for the analysis of each CpG dinucleotide within the sequence according to SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171, and the equivalent positions within SEQ ID NOs: 60- 295, 1029- 1076, 1117 - 1120, 1172 - 1175.

Said oligonucleotides may also be present in the form of peptide nucleic acids. The non-hybridized amplicates are then removed. The hybridized amplicates are then detected. In this context, it is preferred that labels attached to the amplicates are identifiable at each position of the solid phase at which an oligonucleotide sequence is located.

In yet a further embodiment of the method, the genomic methylation status of the CpG positions may be ascertained by means of oligonucleotide probes that are hybridised to the bisulfite treated DNA concurrently with the PCR amplification primers (wherein said primers may either be methylation specific or standard).

A particularly preferred embodiment of this method is the use of fluorescence-based Real Time Quantitative PCR (Heid et al., *Genome Res.* 6:986-994, 1996; also see United States Patent No. 6,331,393) employing a dual-labeled fluorescent oligonucleotide probe (TaqMan™ PCR, using an ABI Prism 7700 Sequence Detection System, Perkin Elmer Applied Biosystems, Foster City, California). The TaqMan™ PCR reaction employs the use of a nonextendible interrogating oligonucleotide, called a TaqMan™ probe, which, in preferred embodiments, is designed to hybridize to a GpC-rich sequence located between the forward and reverse amplification primers. The TaqMan™ probe further comprises a fluorescent "reporter moiety" and a "quencher moiety" covalently bound to linker moieties (e.g., phosphoramidites) attached to the nucleotides of the TaqMan™ oligonucleotide. For analysis of methylation within nucleic acids subsequent to bisulfite treatment, it is required that the probe be methylation specific, as described in United States Patent No. 6,331,393, (hereby incorporated by reference in its entirety) also known as the MethyLight™ assay. Variations on the TaqMan™ detection

methodology that are also suitable for use with the described invention include the use of dual-probe technology (Lightcycler™) or fluorescent amplification primers (Sunrise™ technology). Both these techniques may be adapted in a manner suitable for use with bisulfite treated DNA, and moreover for methylation analysis within CpG dinucleotides.

5 A further suitable method for the use of probe oligonucleotides for the assessment of methylation by analysis of bisulfite treated nucleic acids In a further preferred embodiment of the method, the *fourth step* of the method comprises the use of template-directed oligonucleotide extension, such as MS-SNuPE as described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

10 In yet a further embodiment of the method, the *fourth step* of the method comprises sequencing and subsequent sequence analysis of the amplificate generated in the *third step* of the method (Sanger F., et al., *Proc Natl Acad Sci USA* 74:5463-5467, 1977).

Best mode

15 In the most preferred embodiment of the method the genomic nucleic acids are isolated and treated according to the first three steps of the method outlined above, namely:

a) obtaining, from a subject, a biological sample having subject genomic DNA;

b) extracting or otherwise isolating the genomic DNA;

20 c) treating the genomic DNA of b), or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties; and wherein

d) amplifying subsequent to treatment in c) is carried out in a methylation specific manner, namely by use of methylation specific primers or *blocking oligonucleotides*, and further wherein

25 e) detecting of the amplicates is carried out by means of a real-time detection probe, as described above.

30 Preferably, where the subsequent amplification of d) is carried out by means of methylation specific primers, as described above, said methylation specific primers comprise a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

It is further preferred that, where the subsequent amplification of d) is carried out by means of methylation specific primers, as described above, said methylation specific primers comprise a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

In an alternative most preferred embodiment of the method, the subsequent amplification of d) is carried out in the presence of *blocking oligonucleotides*, as described above. Said *blocking oligonucleotides* comprising a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG, TpG or CpA dinucleotide.

It is particularly preferred that said *blocking oligonucleotides* comprising a sequence having a length of at least 9 nucleotides which hybridizes to a treated nucleic acid sequence according to one of SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG, TpG or CpA dinucleotide.

Step e) of the method, namely the detection of the specific amplicates indicative of the methylation status of one or more CpG positions according to SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO:1171 is carried out by means of real-time detection methods as described above.

Additional embodiments of the invention provide a method for the analysis of the methylation status of genomic DNA according to the invention (SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO:1171 , and complements thereof) without the need for pretreatment.

In the *first step* of such additional embodiments, the genomic DNA sample is isolated from tissue or cellular sources. Preferably, such sources include cell lines, histological slides, body fluids, or tissue embedded in paraffin. In the *second step*, the genomic DNA is extracted. Extraction may be by means that are standard to one skilled in the art, including but not limited to the use of detergent lysates, sonification and vortexing with glass beads. Once the nucleic acids have been extracted, the genomic double-stranded DNA is used in the analysis.

In a preferred embodiment, the DNA may be cleaved prior to the treatment, and this may be by any means standard in the state of the art, in particular with methylation-sensitive restriction endonucleases.

In the *third step*, the DNA is then digested with one or more methylation sensitive restriction enzymes. The digestion is carried out such that hydrolysis of the DNA at the restriction site is informative of the methylation status of a specific CpG dinucleotide.

In the *fourth step*, which is optional but a preferred embodiment, the restriction fragments are amplified. This is preferably carried out using a polymerase chain reaction, and said amplicates may carry suitable detectable labels as discussed above, namely fluorophore labels, radionuclides and mass labels.

In the *fifth step* the amplicates are detected. The detection may be by any means standard in the art, for example, but not limited to, gel electrophoresis analysis, hybridization analysis, incorporation of detectable tags within the PCR products, DNA array analysis, MALDI or ESI analysis.

Subsequent to the determination of the methylation state of the genomic nucleic acids the presence, absence or subclass of prostate cell proliferative disorder is deduced based upon the methylation state of at least one CpG dinucleotide sequence of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences of SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116 and SEQ ID NO: 1171.

Kits

Moreover, an additional aspect of the present invention is a kit comprising, for example: a bisulfite-containing reagent; a set of primer oligonucleotides containing at least two oligonucleotides whose sequences in each case correspond, are complementary, or hybridize under stringent or highly stringent conditions to a 16-base long segment of the sequences SEQ ID NO: 1 to SEQ ID NO: 59, SEQ ID NO: 1017 to SEQ ID NO: 1028, SEQ ID NO: 1116, SEQ ID NO: 1171, SEQ ID NOs: 60- 295, 1029-1076, 1117 – 1120, 1172 – 1175; oligonucleotides and/or PNA-oligomers; as well as instructions for carrying out and evaluating the described method. In a further preferred embodiment, said kit may further comprise standard reagents for performing a CpG position-specific methylation analysis, wherein said analysis comprises one or more of the following techniques: MS-SNuPE, MSP, MethyLight™, HeavyMethyl™, COBRA, and nucleic acid sequencing.

It is further preferred that said comprise a bisulfite-containing reagent; a set of primer oligonucleotides containing at least two oligonucleotides whose sequences in each case correspond, are complementary, or hybridize under stringent or highly stringent conditions to a 16-base long segment of the sequences SEQ ID NO: 1043, 1044, 172, 173, 98, 99, 130, 131, 1172, 1173, 160, 161, 120, 121, 106, 107, 80, 81, 1051, 1052, 66, 67, 1117, 118, 1045, 1046, 1035, 1036, 94, 95, 1033, 1034, 1049, 1050; oligonucleotides and/or PNA-oligomers; as well as instructions for carrying out and evaluating the described method. In a further preferred embodiment, said kit may further comprise standard reagents for performing a CpG position-specific methylation analysis, wherein said analysis comprises one or more of the following techniques: MS-SNuPE, MSP, MethyLight™, HeavyMethyl™, COBRA, and nucleic acid sequencing.

However, a kit along the lines of the present invention can also contain only part of the aforementioned components.

While the present invention has been described with specificity in accordance with certain of its preferred embodiments, the following examples serve only to illustrate the invention and are not intended to limit the invention within the principles and scope of the broadest interpretations and equivalent configurations thereof.

EXAMPLES

In the following EXAMPLES, 'uL' is taken to mean 'microlitre' i.e. 10^{-6} litres, accordingly 'uM' is taken to mean 'micromolar'.

Pooled genomic DNA was isolated and analyzed using the discovery methods, AP-PCR and MCA (Example 1). These technologies distinguish between methylated and unmethylated CpG sites through the use of methylation sensitive enzymes. In general, whole genomic DNA is first digested to increase manageability, and then further digested with a methylation sensitive restriction enzyme. Methylated fragments are preferentially amplified because cleavage at the unmethylated sites prevents amplification of these products. Differentially methylated fragments identified using these techniques are sequenced (Example 2) and compared to the human genome using the BLAST utility in the Ensembl database. The sample set was selected based on the initial aim of the diagnostic problem to be solved, namely the improved detection and discrimination of prostate carcinomas from normal or benign conditions. The following comparisons were run using three "All Cancer" prostate cancer sample pools (10,10, and 20 samples each), two benign prostate hyperplasia (BPH) sample pools (10 samples each), three low grade prostate cancer sample pools (10 samples each), three high grade prostate cancer

sample pools (10 samples each), and one peripheral blood lymphocytes (PBL) pool (9 samples)]:

- BPH vs. All Cancer (High & low Gleason score; transitional (TZ) and peripheral (PZ) zones, 2 comparisons)
- 5' ▪ BPH vs. Low Gleason Score (Gleason < 6, TZ & PZ represented, 2 comparisons)
- BPH vs. High Gleason Score (Gleason > 7, TZ & PZ represented, 2 comparisons)
- Low Gleason Score vs. High Gleason Score (for MCA, each pool was used as tester and driver)
- BPH vs. PBLs
- 10 ▪ All cancer vs. PBLs

The BPH vs. PBLs comparison was not done for APPCR.

For all MCA comparisons that included cancer samples, the cancer was the tester. The low to high Gleason score comparison was run twice, once with low as the tester, and once with high as the tester, bringing the total number of comparisons for MCA to ten. In the experiments
15 with PBLs, the PBL sample was the driver. See Table 1.

Comparison	Nickname	Pool Type	Pool #	Samples per pool	Sample Breakdown			
					Gleas < 6 / Trans. Zone	Gleas < 6 / Periph. Zone	Gleas > 7 Trans. Zone	Gleas > 7 Periph. Zone
BPH vs. All cancers	BA1	BPH	1	10	10 BPH			
		All	1	10	2	3	2	3
BPH vs. All cancers	BA2	BPH	2	10	5 BPH, 5 Normal			
		All	2	10	3	2	3	2
BPH vs. Low	BL1	BPH	1	10	10 BPH			
		Low	1	10	5	5	0	0
BPH vs. Low	BL2	BPH	2	10	5 BPH, 5 Normal			
		Low	2	10	5	5	0	0
BPH vs. High	BH1	BPH	1	10	10 BPH			
		High	1	10	0	0	5	5
BPH vs. High	BH2	BPH	2	10	5 BPH, 5 Normal			
		High	2	10	0	0	5	5
Low vs. High	HL	Low	3	10	5	5	0	0
		High	3	10	0	0	5	5
BPH vs. PBLs	BP	BPH	1	10	10 BPH			
		PBL	1	9	9 PBL's			
Cancer vs. PBL	CP	All	3	20	5	5	5	5
		PBL	1	9	9 PBL's			

TABLE 1: Sample pools used in comparison studies (AP-PCR and MCA)

EXAMPLE 1: MCA and AP-PCR

The aim of the following investigation was to identify one or more *primary* differentially methylated CpG dinucleotide sequences using a controlled assay suitable for identifying at least one differentially methylated CpG dinucleotide sequence within the entire genome, or a representative fraction thereof.

5 All processes were performed on both pooled and/or individual samples, and analysis was carried out using two different Discovery methods; namely, methylated CpG amplification (MCA), and arbitrarily-primed PCR (AP-PCR).

AP-PCR. AP-PCR analysis was performed on sample classes of genomic DNA as follows:

10 1. DNA isolation; genomic DNA was isolated from sample classes using the commercially available Wizard™ kit;

2. Restriction enzyme digestion; each DNA sample pool was digested with 3 different sets of restriction enzymes for 16 hours at 37°C: RsaI (recognition site: GTAC); RsaI (recognition site: GTAC) plus HpaII (recognition site: CCGG; sensitive to methylation); and
15 RsaI (recognition site: GTAC) plus MspI (recognition site: CCGG; insensitive to methylation);

3. AP-PCR analysis; each of the restriction digested DNA samples was amplified with the primers listed in TABLE 2 at a 40°C annealing temperature, and with ³³P dATP in the primer sets outlined in Table 3.

4. Polyacrylamide Gel Electrophoresis; 1.6 µl of each AP-PCR sample was loaded on a
20 5% Polyacrylamide sequencing-size gel, and electrophoresed for 4 hours at 130 Watts. Gels were transferred to chromatography paper, covered with saran wrap, and dried in a gel dryer for a period of about 1-hour.

5. Autoradiographic Film Exposure; film was exposed to dried gels for 20 hours at minus 80°C, and then developed. Glogos II Autorad markers (Stratagene) were added to the
25 dried gel and exposure was repeated with new film. The first autorad was retained for records, while the second was used for excising bands; and

6. Bands corresponding to ~~differential~~ methylation were visually identified on the gel. Such bands were excised and the DNA therein was isolated and cloned using the Invitrogen TA Cloning Kit.

30

TABLE 2: Primers used according to the AP-PCR Protocol Example 1

Name	SEQ ID NO:	Sequence

GC1	928	GGGCCGCGGC
GC2	929	CCCCGCGGGG
GC3	930	CGCGGGGGCG
GC4	931	GCGCGCCGCG
GC5	932	GCGGGGCGGC
G1	933	GCGCCGACGT
G2	934	CGGGACGCGA
G3	935	CCGCGATCGC
G4	936	TGGCCGCCGA
G5	937	TGCGACGCCG
G6	938	ATCCCGCCCG
G7	939	GCGCATGCGG
G8	940	GCGACGTGCG
G9	941	GCCGCGNGNG
G10	942	GCCCGCGNNG
APBS1	943	AGCGGCCGCG
APBS5	944	CTCCCACGCG
APBS7	945	GAGGTGCGCG
APBS10	946	AGGGGACGCG
APBS11	947	GAGAGGCGCG
APBS12	948	GCCCCGCGA
APBS13	949	CGGGGCGCGA
APBS17	950	GGGGACGCGA
APBS18	951	ACCCACCCG

TABLE 3

Combination	primer 1	primer 2	primer 3
101	GC1	G2	APBS1
103	GC3	G4	APBS1
105	GC5	G6	APBS1
107	GC2	G8	APBS5
109	GC4	G10	APBS5
111	GC1	G8	APBS7
113	GC3	G6	APBS7
115	GC5	G4	APBS7

117	GC2	G2	APBS10
119	GC4	G2	APBS10
121	GC1	G4	APBS11
123	GC3	G5	APBS11
125	GC5	G7	APBS11
127	GC2	G9	APBS12
129	GC4	G9	APBS12
131	GC1	G7	APBS13
133	GC3	G5	APBS13
135	GC5	G3	APBS13
137	GC2	G1	APBS17
139	GC4	G3	APBS17
141	GC1	G5	APBS18
143	GC3	G7	APBS18
145	GC5	G9	APBS18
147	G2	G3	APBS17
149	G4	G5	APBS17
151	G6	G7	APBS17
153	G8	G9	APBS13
155	G8	G10	APBS13
157	G6	G8	APBS12
159	G4	G6	APBS12
161	G2	G4	APBS12
163	G2	G10	APBS11
165	G2	G5	APBS11
167	G4	G7	APBS10
169	G6	G9	APBS10
171	G1	G8	APBS10
173	G6	G10	APBS7
175	G4	G8	APBS7
177	G2	G6	APBS5
179	G4	G10	APBS5
181	G2	G8	APBS5
183	APBS1	APBS10	APBS11
185	APBS5	APBS7	APBS17
187	APBS1	APBS12	APBS18
189	APBS10	APBS13	APBS17
191	APBS5	APBS11	APBS12
193	APBS7	APBS10	APBS13
195	APBS1	APBS5	APBS11
197	APBS7	APBS17	APBS18
199	APBS1	APBS12	APBS13

MCA. MCA was used to identify hypermethylated sequences in one population of genomic DNA as compared to a second population by selectively eliminating sequences that do not contain the hypermethylated regions. This was accomplished, as described in detail herein above, by digestion of genomic DNA with a methylation-sensitive enzyme that cleaves un-

methyated restriction sites to leave blunt ends, followed by cleavage with an isoschizomer that is methylation insensitive and leaves sticky ends. This is followed by ligation of adaptors, amplicon generation and subtractive hybridization of the tester population with the driver population.

5 The initial restriction digestion reaction solutions contained the following:

DRIVERS:

	DNA	510 uL
	buffer 4	60 uL
10	100x BSA	6 uL
	SmaI (20U/uL)	24 uL

TESTERS:

	DNA	68 uL
15	buffer 4	10 uL
	10x BSA	10 uL
	SmaI (20U/uL)	2 uL

The reaction mixtures were incubated overnight at room temperature.

The pools were then further digested with Xma I (2 uL=100 U), 6 hours at 37°C. 2 uL
20 (20U) XmaI was added to each tester digest and 8 uL (80U) to each driver digest

The cleaned-up, digested material was ligated to the adapter-primer RXMA24 + RXMA12 (Sequence: RXMA24: AGCACTCTCCAGCCTCTCACCGAC (SEQ ID NO: 952); RXMA12: CCGGGTCGGTGA (SEQ ID NO:953). These were hybridized to create the adapter by heating together at 70°C and slowly cooling to room temperature (RT) in a 30 uL reaction:

25	Each DNA	33 uL
	T4 Buffer	6 uL
	RXMA adapter-primer (100 uM)	20 uL
	Ligase	1 uL

30

The reaction solution was incubated overnight at room temperature.

3 uL of the ligation mix for both tester and driver populations was used in each initial PCR to generate the starting amplicons. The reaction solutions were as follows:

TESTERS:

	100uM RXMA24	1 uL
	PCR buffer	10 uL
	25 mM dNTPs	1.2 uL
5	ddH2O	68.8 uL
	Titanium Taq	1 uL
	100% DMSO	2 uL
	5M Betaine	10 uL
10	3 uL ligated tester DNA was added to each 97 uL tester cocktail.	

DRIVERS:

Drivers are amplified with dUTP in place of dTTP:

	100uM RXMA24	1 uL
15	PCR buffer	10 uL
	25 mM dNTPs	1.2 uL (25 mM each dATP, dCTP, dGTP, and dUTP)
	ddH2O	68.8 uL
	Titanium Taq	1 uL
	100% DMSO	2 uL
20	5M Betaine	10 uL

3 uL ligated driver DNA was added to each 97 uL driver cocktail.

PCR conditions:

25	72 degrees 5 min
	30 cycles:
	95 degrees 1 min
	72 degrees 3 min
	Final extension:
30	72 degrees 10 min.

The tester amplicons were then digested with XmaI, yielding overhanging ends, and the driver amplicons were digested with SmaI, yielding blunt end fragments.

DRIVERS (SmaI):

	DNA	500 uL
	Buffer 4	100 uL
	100x BSA	10 uL
5	H2O	340 uL
	SmaI (20U/uL)	50 uL
Total vol: 1 mL. Incubated overnight at room temp.		

TESTERS (XmaI):

10	DNA	20 uL
	buffer 4	10 uL
	10x BSA	10 uL
	H2O	59 uL
	XmaI (50U/uL)	1 uL
15	Total vol: 100 uL. Incubated overnight at 37 degrees.	

A new set of adapter primers (hybridized as described for the above RXMA primers) JXMA24 + JXMA12 (Sequence: JXMA24: ACCGACGTCGACTATCCATGAACC (SEQ ID NO:954); JXMA12: CCGGGGTTCATG (SEQ ID NO:955) was ligated to the Tester in a Thermocycler at 16°C for 2 hours in the following reaction solution:

20	DNA	16 uL
	T4 buffer	3 uL
	JXMA-P adapter (100uM)	10 uL
	T4 Ligase (400U/uL)	1 uL

25

The digested tester and driver amplicons were hybridized together. A selective PCR reaction was done using primer JXMA24 (SEQ ID NO:954). The reaction solution contained:

	JXMA24	0.5 uL
30	taq buffer	5 uL
	dNTPs	0.6 uL
	ddH2O	27.4 uL
	betaine	5 uL
	DMSO	1 uL

Titanium taq 0.5 uL
DNA 10 uL

PCR conditions:

- 5 72 degrees 8 min (fill in ends)
 5 cycles:
 95 degrees 1 min
 72 degrees 3 min
 final extension:
10 72 degrees 10 min

Subsequently, 20 uL of Mung Bean nuclease buffer plus 10 uL Mung Bean Nuclease (10U) was added and incubated at 37°C for 30 minutes. This reaction was cleaned up and used as a template for 25 more cycles of PCR using JXMA24 primer in the following reaction

- 15 solution:
 JXMA24 1 uL
 taq buffer 10 uL
 dNTPs 1.2 uL
 ddH2O 27 uL
20 betaine 10 uL
 DMSO 2 uL
 Titanium taq 1 uL
 DNA 48 uL

under the following conditions.

- 25 95 degrees 2 min
 30 cycles:
 95 degrees 1 min
 72 degrees 3 min
 Final extension:
30 72 degrees 10 min
 Hold at 4 degrees

The resulting PCR product (tester) was digested again using XmaI:
45 uL DNA

15 uL Buffer 4
 15 uL 10x BSA
 71 uL H₂O
 4 uL XmaI

5 Incubated overnight at 37 degrees

A third adapter, NXMA24 (AGGCAACTGTGCTATCCGAGTGAC; SEQ ID NO:956) + NXMA12 (CCGGGTCACTCG; SEQ ID NO: 957) was ligated. The tester (500 ng) was hybridized a second time to the original digested driver (40 ug) in 4 uL EE (30 mM EPPS, 3 mM EDTA) and 1 uL 5 M NaCl at 67°C for 20 hours. Selective PCR was performed using NXMA24 primer as follows:

	NXMA24	0.5 uL
	taq buffer	5 uL
15	dNTPs	0.6 uL
	ddH ₂ O	27.4 uL
	betaine	5 uL
	DMSO	1 uL
	Titanium taq	0.5 uL
20	DNA	10 uL

PCR program:

72 degrees 8 min (fill in ends)

8 cycles:

25 95 degrees 1 min

72 degrees 3 min

final extension:

72 degrees 10 min

The reaction solution was held at 4 degrees

30 Subsequently, 20 uL of Mung Bean nuclease buffer plus 10 uL Mung Bean Nuclease (10U) was added and incubated at 30°C for 30 minutes. This reaction was cleaned up and used as a template for 25 more cycles of PCR using NXMA24 primer as follows:

Reaction solution

	NXMA24	1 uL
	taq buffer	10 uL
	dNTPs	1.2 uL
	ddH2O	27 uL
5	betaine	10 uL
	DMSO	2 uL
	Titanium taq	1 uL
	DNA	48 uL

- 10 PCR program:
 95 degrees 2 min
 30 cycles:
 95 degrees 1 min
 72 degrees 3 min
- 15 Final extension:
 72 degrees 10 min
 Hold at 4 degrees

The resulting PCR product was digested with XmaI :

- 20 Reaction solution:
- | | |
|----------|-------|
| DNA | 38 uL |
| buffer 4 | 5 uL |
| 10x BSA | 5 uL |
| Xma I | 2 uL |

- 25 Incubated overnight at 37 degrees.

- 30 The DNA digest was then ligated into the vector pBC Sk— predigested with XmaI and phosphatased (675 ng). 5 uL of the ligation mixture was used to transform chemically competent TOP10™ cells according to the manufacturer's instructions. The transformations were plated onto LB/XGal/IPTG/CAM plates. Selected insert colonies were sequenced according to Example 2.

Example 1 resulted in a large number of unique sequences that were potential candidates for assay markers. A subset of these sequences was eliminated due their high (>50%) repeat content. A total of 480 unique sequences were identified in the comparisons performed for this study. A subset of these sequences were further selected using the following scoring procedure:

Appearance using multiple methods

Appearance in multiple pools

Located within CpG island

Located within the promoter region of a gene

Near or within predicted or known gene

Known to be associated with disease

Class of gene (transcription factor, growth factor, etc.)

Repetitive element (negative score)

Under this scoring scheme, a MeST sequence receives a point for each of the above criteria, and receives a score of (-)8 for having repetitive sequence content greater than 50%. The highest score possible is 7, the lowest is (-)8. Scores are automatically generated using a proprietary database. Of the initial set of 480 MeST sequences, 277 scored 0 or higher. Using the scoring criteria above, along with manual review of the sequences, the number of candidate MeST was further reduced to 126 unique sequences.

Primer design for the 126 sequences was then initiated for the purpose of bisulfite sequencing. Thirty five of the sequences were discarded for various reasons including inability to design adequate primers, failure of amplification from control DNA, or if further scrutiny of the sequence or updates of the Ensembl database revealed poor quality or repeat sequences not previously noted.

EXAMPLE 2: Bisulfite Sequencing

For bisulfite sequencing amplification primers were designed to cover each identified MeST sequence when possible or part of the 1000 bp upstream or 1000 bp downstream flanking regions surrounding the position. Samples used in Example 1 were utilized for amplicon production in this phase of the study. Each sample was treated with sodium bisulfite and sequenced. Sequence data was obtained using ABI 3700 sequencing technology. Obtained sequence traces were normalized and percentage methylation calculated using Epigenomic's proprietary ESME bisulphite sequence sequencing trace analysis program.

Results of bisulfite sequencing

The following properties were noted:

1. Bisulfite sequencing indicates differential methylation of a CpG site between selected classes of samples (fisher score)
2. Co-methylation is observed

- Genomic regions that were considered to demonstrate significant co-methylation as assessed by these criteria then proceeded to further investigation.

Figure 1 shows the sequencing data of a fragment of the gene Prostaglandin E2 Receptor, EP4 Subtype. Here, bisulfite sequencing showed differential but non-conclusive patterns of methylation between samples. The gene was further investigated on a larger sample set using the array process (Example 3) as the accuracy of this gene as a marker could be improved when analysed in combination with other genes.

Figure 3 shows the sequencing data of a fragment of the gene 1-Acyl-SN-Glycerol-3-Phosphate Acyltransferase Gamma. This was representative of a subset of ROIs for which only poor quality sequence reads were obtained and the gene was only able to be meaningfully analysed using the array process (Example 3).

A selection of the differentially methylated genomic regions were further analysed by means of high throughput array analysis. The most useful final assay suitable for a diagnostic/classification screening test would enable analysis of body fluids such as serum, plasma or urine sediment (obviating the need for invasive procedures). Therefore, the sample set included DNA samples from other cancers which may be present in blood to provide more specific marker sets for sensitive assays.

11

Description of sample set for chip study

The sample set for the microarray analysis was designed to provide information concerning both the sensitivity and specificity of the marker candidates. A large number of samples (Table 7) from prostate cancer, BPH and normal prostate were screened. Prostate cancer samples were grouped by Gleason Score (High (≥ 8), Moderate (7), and Low (≤ 6)) and by zone (peripheral or transitional). The distribution of BPH samples was random, but because most BPH is derived from the transitional zone, it can be assumed that most samples were of that origin. In addition to prostate samples, a number of other cancer types were included to test for specificity to the prostate. PBL samples were included to analyze the potential use of these markers in a blood based screen. Normal liver and liver cancer were also included because of the observed methylation of GSTP1 in these samples.

TABLE 7. Overview of samples for the array study.

Sample Type	Sample Type
Prostate Cancers	Endocrine Related Cancers
<ul style="list-style-type: none"> • High Grade (Gleason ≥ 8) • Transitional Zone • Peripheral Zone • Low Grade (Gleason ≤ 6) • Transitional Zone • Peripheral Zone • Moderate Grade (Gleason = 7) • Transitional Zone • Peripheral Zone • Additional Prostate Cancers • Post hormone therapy 	<ul style="list-style-type: none"> • Breast • Male • Female • Ovarian • Uterine
Benign Prostate Disease	Other Cancers
<ul style="list-style-type: none"> • BPH • Benign Fibroma 	<ul style="list-style-type: none"> • Liver • Lung • Esophageal • Salivary Gland • Stomach • Pancreatic • Melanoma • Colon

Genitourinary Tract Cancers	Other Normal tissues
<ul style="list-style-type: none"> • Prostatitis • Bladder • Testicular • Kidney 	<ul style="list-style-type: none"> • Prostate • Transitional • Peripheral • Bladder • Kidney • Liver • Testes • Sperm • Ureter • PBLs

DNA extraction

Samples were received from either as frozen tissue or extracted genomic DNA. All DNA samples were extracted using Qiagen Genomic Tip-500 columns or the MagnaPure device.

5 Bisulfite treatment and multiplex PCR

Total genomic DNA of all samples was bisulfite treated to convert unmethylated cytosines to uracil. Methylated cytosines remained conserved as cytosines. Bisulfite treatment was performed using Epigenomics' proprietary bisulfite treatment process. Two independent bisulfite reactions were performed per patient sample. After bisulfitation 10 ng of each DNA sample was used in subsequent multiplex PCR (mPCR) reactions containing 7-8 primer pairs.

Hybridization

Each reaction contained the following:

0.4 mM each dNTPS

1 Unit Taq Polymerase

15 2.5 ul PCR buffer

3.5 mM MgCl₂

80 nM Primerset (12-16 primers)

11.25 ng DNA (bisulfite treated)

Further details of the primers are shown in TABLE 8.

Forty cycles were carried out as follows: Denaturation at 95°C for 15 min, followed by annealing at 55°C for 45 sec., primer elongation at 65°C for 2 min. A final elongation at 65°C was carried out for 10 min.

Hybridization

5 All PCR products from each individual sample were then hybridised to glass slides carrying a pair of immobilised oligonucleotides for each CpG position under analysis. Each of these detection oligonucleotides was designed to hybridize to the bisulphite converted sequence around one CpG site which was either originally unmethylated (TG) or methylated (CG). See Table 2 for further details of all hybridization oligonucleotides used (both informative and non-
10 informative). Hybridization conditions were selected to allow the detection of the single nucleotide differences between the TG and CG variants.

5 ul volume of each multiplex PCR product was diluted in 10 x SSARC buffer. The reaction mixture was then hybridized to the detection oligonucleotides as follows. Denaturation at 95°C, cooling down to 10°C, hybridization at 42°C overnight followed by washing with 10 x
15 SSARC and dH₂O at 42°C.

Further details of the hybridization oligonucleotides are shown in TABLE 9.

Fluorescent signals from each hybridized oligonucleotide were detected using genepix scanner and software. Ratios for the two signals (from the CG oligonucleotide and the TG oligonucleotide used to analyse each CpG position) were calculated based on comparison of
20 intensity of the fluorescent signals.

For each patient, 2 DNA aliquots were bisulfite treated and for each bisulfite treated DNA sample two hybridizations were performed, resulting in a total of 4 chips processed per patient. For hybridization, the samples were grouped into 2 processing rounds in order to avoid a potential process-bias. As stated, each of the 2 rounds included a 2 fold redundancy for each
25 DNA sample for the 4-fold redundancy per patient. The samples were hybridized in batches of 112 samples randomized for sex, diagnosis, tissue, and bisulfite batch.

Data analysis methods:

30 Analysis of the chip data

For the analysis of the chip data Epigenomics' proprietary software "EpiScape[®]" was used. It encompasses a variety of statistical tools and novel machine learning methods for analyzing and visualizing methylation array data. In the following sections we summarize the most important data analysis techniques that we applied for analyzing the data.

5

From raw hybridization intensities to methylation ratios

The log methylation ratio ($\log(\text{CG}/\text{TG})$) at each CpG position is determined according to a standardized preprocessing pipeline. This log ratio has the property that the hybridization noise has approximately constant variance over the full range of possible methylation rates.

10

Hypothesis testing

Our main task was to identify markers that can make a significant contribution to the class prediction of samples. For the 'particularly preferred embodiments' of the invention the significant contribution was detected when the null-hypothesis that a prediction model including the marker does not improve classification performance over a model without the marker could be rejected with $p < 0.05$. Because we applied this test to a whole set of potential markers, we corrected the p-values for multiple testing. We did this by applying the conservative Bonferroni correction, which simply multiplies the single marker p-values with the number of potential markers tested. We also gave results with the less conservative False Discovery Rate (FDR) method.

20

Throughout this example a marker (sometimes also simply referred to as gene or amplicon) is also referred to as a genomic region of interest (ROI). It comprises of several CpG positions in the respective genomic region. For testing the null hypothesis that a marker has no predictive power we used the likelihood ratio test for logistic regression models. The logistic regression model for a single marker is a linear combination of methylation measurements from all CpG positions in the respective ROI. The fitted logistic regression model is compared to a constant probability model that is independent of methylation and represents the null hypothesis. The p-value of the marker was computed via the likelihood ratio test.

25

A significant p-value for a marker means that the methylation of this ROI has some systematic correlation to the question of interest as given by the two classes. In general a significant p-value does not necessarily imply a good classification performance. However, because with logistic regression we used a linear predictor as the basis of our test statistic small p-values are indicative of a good clinical performance.

30

Class prediction by supervised learning

To give a reliable estimate of how well the CpG ensemble of a selected marker can differentiate between different tissue classes we can determine its prediction accuracy by classification. For that purpose we calculated a methylation profile-based prediction function using a certain set of tissue samples with a specific class label. This step is called training and it exploits the prior knowledge represented by the data labels. The prediction accuracy of that function was then tested on a set of independent samples. As a method of choice, we used the support vector machine (SVM) algorithm to learn the prediction function. In this analysis, sensitivity and specificity were weighted equally. This was achieved by setting the risk associated with false positive and false negative classifications to be inversely proportional to the respective class sizes. Therefore sensitivity and specificity of the resulting classifier could be expected to be approximately equal. Note that this weighting can be adapted according to the clinical requirements.

Estimating the performance of the tissue class prediction: Cross Validation

With limited sample size the cross-validation method provided an effective and reliable estimate for the prediction accuracy of a discriminator function, and therefore in addition to the significance of the markers we provided cross-validation accuracy, sensitivity and specificity estimates. For each classification task, the samples were partitioned into 5 groups of approximately equal size. Then the learning algorithm was trained on 4 of these 5 sample groups. The predictor obtained by this method was then tested on the remaining group of independent test samples. The number of correct positive and negative classifications was counted over 10 runs for the learning algorithm for all possible choices of the independent test group without using any knowledge obtained from the previous runs. This procedure was repeated on 10 random permutations of the sample set giving a better estimate of the prediction performance than if performed by simply splitting the samples into one training sample set and one independent test set.

Data analysis results

Our first step in analysis of the array data was to look at discriminatory markers in a comparison of all tissues of prostatic origin. We first compared normal and BPH prostate tissue against prostate cancer samples, and found that many of the markers used in this study have p-values meeting the desired criteria (Figure 4). Next, we compared prostate cancer tissues to all

other tissue classes used in this study (Table 7). Almost all markers met the specified statistical criteria with this sample set. The GSTP1 gene is known to be hypermethylated in prostate cancer, but also displays hypermethylation in other cancers. Therefore, our final comparison was a more detailed examination of the methylation levels in prostate cancer versus other cancer types.

Prostate Normal and BPH vs. Prostate Cancer

In this comparison, the negative class consisted of 91 samples from normal prostate, and BPH. The positive class consisted of 99 prostate cancer samples. Most of the markers met the criteria of $p\text{-value} < 0.05$ (Figure 4). The p-values, accuracy, sensitivity and specificity of the analysis are shown in Table 4. The best 12 markers are further shown in Figure 5.

Prostate Normal and Other Tissues vs. Prostate Cancer

Comparisons were then performed on the complete sample set. The negative group was expanded to include normal tissue from other organs and cancer of other origins than prostate, according to TABLE 7. The negative class consists of 254 samples from normal prostate, BPH and other normal and cancerous tissues. The positive class consists of 99 prostate cancer samples. Again the p-values for most markers meet the significance level of $p = < 0.05$ (Table 5). The accuracy of the highest performing marker is ~ 86% (see figure 6 and/or Table 5). The p-values, accuracy, sensitivity and specificity of the analysis are shown in Table 5. The best 12 markers are further shown in Figure 7.

Other Cancers vs. Prostate Cancer

Since hypermethylation of GSTP1 (state of the art methylation prostate cancer marker) is not specific to the prostate, we examined the methylation status of prostate cancer and other cancers in greater detail. Figure 16 shows that GSTP1 (SEQ ID NO:57) was strongly hypermethylated in liver cancer and to a lesser degree in breast cancer. Nevertheless, several other of the best candidate markers distinguish well between cancer of the prostate and liver. The p-values, accuracy, sensitivity and specificity of the analysis are shown in Table 6. The best 12 markers are further shown in Figure 8.

Tables 4-6 below summarize the performance characteristics of all markers in the following comparisons of tissues: Normal Prostate and BPH vs. Prostate Cancer (Table 4); Normal Prostate, BPH and other tissues vs. Prostate Cancer (Table 5); and Other Cancer Tissues vs. Prostate Cancer (Table 6).

The analyses in Tables 4 and 5 contained BPH and normal prostate samples in the analysis group. The analysis for Normal Prostate and BPH vs. Prostate Cancer was designed to determine the performance of the markers in a prostate specific environment. The analysis that included other tissues, both cancer and normals (Normal Prostate, BPH and Other Tissues vs. Prostate Cancer) took into consideration the performance of the markers with a background that may contribute or alter the overall performance of the markers in remote samples.

Cancer types (Table 6) were also compared because of the propensity for GSTP1 to be methylated in multiple cancer types. This type of lack of specificity could have a negative impact on the performance of a marker in body fluid-based assays. GSTP1 (SEQ ID NO: 57) is highly methylated in prostate cancer, but also in liver cancer as anticipated. IGF2 (SEQ ID NO: 58) is similarly methylated in liver cancer. The majority of the markers shown in Figure 8 are unmethylated in most cancer types, with the exception of prostate cancer. From Figures 4-8, it can be observed that there are multiple candidates that have the potential to be informative and accurate markers. It is recommended that multiple markers be combined to ensure a high sensitivity and specificity.

TABLE 4: Normal Prostate, BPH and Other Tissues vs. Prostate Cancer

Genomic SEQ ID NO:	Treated Methylated sense strand SEQ ID NO:	Treated Methylated Antisense strand SEQ ID NO:	Treated Unmethylate d SEQ ID NO:	Treated Unmethylate d antisense sense strand SEQ ID NO:	P-value	Accurac y	Sensitivit y	Specificit y
57	172	173	290	291	1.30E-027	0.86	0.67	0.93
23	104	105	222	223	2.00E-029	0.81	0.75	0.83
36	130	131	248	249	3.80E-018	0.75	0.75	0.76
56	170	171	288	289	1.10E-012	0.74	0.62	0.79
11	80	81	198	199	5.10E-019	0.74	0.76	0.74
20	98	99	216	217	4.90E-016	0.73	0.77	0.71
22	102	103	220	221	1.10E-009	0.7	0.61	0.74
31	120	121	238	239	6.90E-018	0.7	0.79	0.66
30	118	119	236	237	1.60E-012	0.69	0.81	0.64
58	174	175	292	293	1.20E-011	0.68	0.71	0.67
34	126	127	244	245	5.50E-009	0.68	0.65	0.69
41	140	141	258	259	1.50E-008	0.67	0.7	0.66
59	176	177	294	295	4.90E-007	0.67	0.59	0.7
51	160	161	278	279	1.50E-012	0.67	0.76	0.63
24	106	107	224	225	1.30E-006	0.67	0.67	0.67

18	94	95	212	213	1.10E-014	0.67	0.84	0.6
54	166	167	284	285	3.80E-007	0.66	0.7	0.65
27	112	113	230	231	6.60E-007	0.66	0.7	0.64
7	72	73	190	191	8.30E-005	0.65	0.62	0.67
35	128	129	246	247	1.00E-004	0.65	0.53	0.69
16	90	91	208	209	7.50E-011	0.64	0.77	0.6
38	134	135	252	253	1.20E-004	0.64	0.63	0.64
14	86	87	204	205	5.20E-008	0.63	0.72	0.6
25	108	109	226	227	3.50E-011	0.62	0.79	0.56
1	60	61	178	179	8.20E-005	0.62	0.67	0.6
28	114	115	232	233	1.40E-003	0.62	0.67	0.59
43	144	145	262	263	3.70E-002	0.61	0.56	0.63
4	66	67	184	185	4.40E-004	0.61	0.64	0.59
26	110	111	228	229	5.60E-003	0.6	0.64	0.59
12	82	83	200	201	3.00E-004	0.58	0.75	0.52
21	100	101	218	219	1.80E-002	0.57	0.64	0.54
33	124	125	242	243	1.10E-002	0.56	0.66	0.53

TABLE 5: Normal Prostate and BPH vs. Prostate Cancer

Genomic SEQ ID NO:	Treated methylate d sense strand SEQ ID NO:	Treated methylate d antisense strand SEQ ID NO:	Treated unmethylate d sense strand SEQ ID NO:	Treated unmethylate d antisense strand SEQ ID NO:	P-value	Accu racy	Sensi tivity	Spe cific ity
57	172	173	290	291	4.60E-023	0.85	0.77	0.93
36	130	131	248	249	8.10E-019	0.81	0.75	0.86
23	104	105	222	223	6.10E-019	0.8	0.75	0.85
34	126	127	244	245	3.10E-015	0.78	0.71	0.86
20	98	99	216	217	1.60E-016	0.78	0.75	0.8
31	120	121	238	239	5.20E-015	0.76	0.71	0.81
59	176	177	294	295	1.90E-014	0.76	0.68	0.84
56	170	171	288	289	2.00E-013	0.76	0.65	0.53
30	118	119	236	237	5.90E-011	0.75	0.76	0.75
48	154	155	272	273	2.70E-011	0.74	0.71	0.78
54	166	167	284	285	1.20E-009	0.74	0.72	0.76
11	80	81	198	199	1.00E-010	0.74	0.69	0.8
24	106	107	224	225	1.10E-011	0.72	0.67	0.78
14	86	87	204	205	3.50E-009	0.71	0.63	0.8
18	94	95	212	213	3.10E-010	0.71	0.76	0.66
28	114	115	232	233	7.80E-008	0.71	0.69	0.72

8	74	75	192	193	4.10E-008	0.7	0.72	0.68
7	72	73	190	191	3.00E-004	0.7	0.62	0.78
4	66	67	184	185	6.30E-009	0.69	0.66	0.72
35	128	129	246	247	1.40E-008	0.69	0.59	0.8
27	112	113	230	231	1.40E-006	0.69	0.68	0.7
58	174	175	292	293	8.90E-006	0.68	0.65	0.71
26	110	111	228	229	1.20E-008	0.68	0.69	0.66
22	102	103	220	221	3.40E-008	0.67	0.57	0.78
41	140	141	258	259	7.90E-005	0.66	0.67	0.66
37	132	133	250	251	1.70E-006	0.66	0.6	0.73
1	60	61	178	179	7.40E-005	0.66	0.72	0.6
49	156	157	274	275	1.80E-005	0.66	0.62	0.71
16	90	91	208	209	1.30E-003	0.65	0.67	0.62
2	62	63	180	181	1.50E-002	0.64	0.66	0.63
44	146	147	264	265	7.50E-004	0.64	0.67	0.6
32	122	123	240	241	2.50E-003	0.64	0.59	0.69
13	84	85	202	203	5.10E-002	0.63	0.61	0.66
47	152	153	270	271	2.00E-002	0.63	0.64	0.61
42	142	143	260	261	3.30E-003	0.62	0.67	0.57
55	168	169	286	287	7.10E-003	0.62	0.67	0.57
29	116	117	234	235	5.10E-002	0.62	0.64	0.59
3	64	65	182	183	1.30E-001	0.61	0.59	0.64
50	158	159	276	277	1.00E+000	0.6	0.64	0.56
51	160	161	278	279	2.90E-002	0.6	0.65	0.56
43	144	145	262	263	9.60E-002	0.6	0.6	0.61
21	100	101	218	219	6.20E-001	0.59	0.66	0.52
46	150	151	268	269	3.00E-001	0.59	0.59	0.59
10	78	79	196	197	5.50E-001	0.59	0.52	0.66
38	134	135	252	253	5.10E-001	0.58	0.55	0.62
25	108	109	226	227	1.20E-002	0.57	0.52	0.63
15	88	89	206	207	1.00E+000	0.56	0.48	0.65
6	70	71	188	189	1.00E+000	0.56	0.63	0.48
33	124	125	242	243	1.00E+000	0.55	0.43	0.68
5	68	69	186	187	1.00E+000	0.55	0.6	0.5
9	76	77	194	195	1.00E+000	0.55	0.53	0.56
52	162	163	280	281	1.00E+000	0.54	0.48	0.6
40	138	139	256	257	1.00E+000	0.53	0.48	0.58
45	148	149	266	267	1.00E+000	0.52	0.38	0.68
17	92	93	210	211	1.00E+000	0.52	0.58	0.46
12	82	83	200	201	1.00E+000	0.47	0.36	0.58
39	136	137	254	255	1.00E+000	0.45	0.46	0.45
19	96	97	214	215	1.00E+000	0.4	0.46	0.32

TABLE 6: Other cancers vs. Prostate cancer

Genomic SEQ ID NO:	Treated methylated sense strand SEQ ID NO:	Treated methylated antisense strand SEQ ID NO:	Treated unmethylate d sense strand SEQ ID NO:	Treated unmethylate d antisense strand SEQ ID NO:	p-value	accuracy	sensitivit y	specificit y
-----------------------	--------------------------------------------------------	------------------------------------------------------------	-----------------------------------------------------------	---------------------------------------------------------------	---------	----------	-----------------	-----------------

57	172	173	290	291	9.7e-14	0.80	0.70	0.89
23	104	105	222	223	2.4e-19	0.78	0.75	0.81
25	108	109	226	227	6.9e-16	0.75	0.85	0.65
11	80	81	198	199	2.0e-13	0.75	0.76	0.73
51	160	161	278	279	2.0e-12	0.74	0.79	0.69
31	120	121	238	239	1.5e-13	0.74	0.92	0.58
16	90	91	208	209	1.1e-14	0.73	0.82	0.66
30	118	119	236	237	2.4e-08	0.73	0.82	0.64
10	78	79	196	197	5.5e-11	0.72	0.83	0.63
41	140	141	258	259	9.4e-07	0.70	0.73	0.66
18	94	95	212	213	5.0e-09	0.69	0.83	0.57
14	86	87	204	205	2.8e-09	0.69	0.86	0.55
20	98	99	216	217	9.2e-07	0.68	0.78	0.60
12	82	83	200	201	9.7e-07	0.68	0.76	0.61
36	130	131	248	249	6.1e-08	0.67	0.74	0.62
38	134	135	252	253	3.8e-05	0.67	0.66	0.69
22	102	103	220	221	4.1e-05	0.67	0.62	0.71
58	174	175	292	293	1.6e-08	0.66	0.73	0.61
46	150	151	268	269	6.6e-08	0.66	0.87	0.48
56	170	171	288	289	4.6e-05	0.66	0.60	0.72
27	112	113	230	231	1.4e-02	0.65	0.69	0.62
21	100	101	218	219	5.6e-05	0.64	0.70	0.59
15	88	89	206	207	4.5e-05	0.63	0.85	0.43
5	68	69	186	187	4.4e-06	0.63	0.73	0.54
42	142	143	260	261	2.8e-04	0.62	0.77	0.49
34	126	127	244	245	6.8e-03	0.62	0.70	0.55
7	72	73	190	191	3.0e-03	0.62	0.56	0.66
33	124	125	242	243	7.6e-02	0.61	0.72	0.52
28	114	115	232	233	7.2e-01	0.60	0.73	0.49
6	70	71	188	189	2.8e-01	0.60	0.65	0.55
1	60	61	178	179	9.5e-02	0.59	0.60	0.58
59	176	177	294	295	5.1e-02	0.59	0.62	0.56
43	144	145	262	263	4.2e-01	0.59	0.58	0.60
24	106	107	224	225	1.3e-01	0.59	0.76	0.43
37	132	133	250	251	1.1e-01	0.59	0.69	0.49
48	154	155	272	273	5.8e-01	0.59	0.72	0.47
4	66	67	184	185	4.2e-02	0.58	0.71	0.48
45	148	149	266	267	1.0e+00	0.58	0.79	0.40
39	136	137	254	255	3.1e-02	0.58	0.55	0.61
55	168	169	286	287	1.0e+00	0.58	0.69	0.48
26	110	111	228	229	7.3e-02	0.58	0.67	0.49
2	62	63	180	181	1.0e+00	0.57	0.63	0.52
54	166	167	284	285	8.2e-01	0.57	0.68	0.47
49	156	157	274	275	5.9e-02	0.56	0.82	0.34
8	74	75	192	193	1.0e+00	0.56	0.61	0.51
13	84	85	202	203	1.0e+00	0.56	0.59	0.53
32	122	123	240	241	1.0e+00	0.55	0.63	0.49
29	116	117	234	235	1.0e+00	0.55	0.55	0.55
19	96	97	214	215	1.0e+00	0.55	0.54	0.55

47	152	153	270	271	1.0e+00	0.54	0.84	0.29
9	76	77	194	195	9.7e-02	0.54	0.55	0.53
50	158	159	276	277	1.0e+00	0.54	0.62	0.47
52	162	163	280	281	1.0e+00	0.54	0.51	0.56
17	92	93	210	211	1.0e+00	0.54	0.49	0.57
44	146	147	264	265	1.0e+00	0.53	0.60	0.47
35	128	129	246	247	1.0e+00	0.52	0.45	0.59
3	64	65	182	183	1.0e+00	0.52	0.59	0.45
40	138	139	256	257	1.0e+00	0.51	0.56	0.47

TABLE 7 is to be found at the beginning of Example 3.

TABLE 8

<i>Name and /or SEQ ID No:</i>	<i>Primer:</i>	<i>Amplifica te Length:</i>
(SEQ ID NO: 1)	TGGTATAGGAGGAGAAGAGTTG (SEQ ID NO: 296) TCAATCCCTAAAACCCAAA (SEQ ID NO: 297)	327
(SEQ ID NO: 2)	ACCCAACTAACAATCAAAAAT (SEQ ID NO: 299) GGAAGGGAAGGATGAGAGTAT (SEQ ID NO: 298)	326
(SEQ ID NO: 3)	GGAAGGTTTAAGGTGAGAGAA (SEQ ID NO: 300) CAAAATAACCAATCCCCTAAA (SEQ ID NO: 301)	339
LIM/HOMEOBOX PROTEIN LHX9 (SEQ ID NO: 4)	CCCCAATATAAATCTACCAACC (SEQ ID NO: 303) TTATTTGAATTTTGGAGGTTATG (SEQ ID NO: 302)	372
(SEQ ID NO: 5)	TTAATGAAGTAGGGTTTGTATTGT (SEQ ID NO: 304) CCTCCAAAATCTTAACCAAAT (SEQ ID NO: 305)	421
(SEQ ID NO: 6)	CCCAACTAACTCAAATTCCAC (SEQ ID NO: 307) TTTATTTTAGGAGGGAAGGATT (SEQ ID NO: 306)	434
(SEQ ID NO: 7)	GTGGTTTTGGGGAATTAGTAT (SEQ ID NO: 308) CTCCTACATATCCCATCTCATC (SEQ ID NO: 309)	483
UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR	AATTAAGGTTTAGGGTTTTGTTT (SEQ ID NO: 310) ACCTTCCTACAAATCTACCTAC	365

Name and /or SEQ ID No:	Primer:	Amplifica te Length:
(UBIQUITIN- HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	(SEQ ID NO: 311)	
BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATAGTTTTGTGGGTTTAAGAGG (SEQ ID NO: 312) ACCCTAACCTTATACAATACCAAC (SEQ ID NO: 313)	414
BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GGTGGGGTTATTAAGGAGTTTA (SEQ ID NO: 314) CTCAACTACCATACCCAAAAA (SEQ ID NO: 315)	480
(SEQ ID NO: 10)	TTGTGTTGGTTGTAAAAGGA (SEQ ID NO: 316) CAAACACTATACACCTCTCAACA (SEQ ID NO: 317)	428
(SEQ ID NO: 11)	TTGAGGTTATTGGTTTATAGATTTT (SEQ ID NO: 318) CCCTAACCACCCCTTCTA (SEQ ID NO: 319)	457
(SEQ ID NO: 12)	ACTCCATACACTTTTACCAACC (SEQ ID NO: 321) TGTGTGAAATGTTTTAGTTTAATTG (SEQ ID NO: 320)	455
HOOK2 PROTEIN (SEQ ID NO: 13)	TGTGTTAGGAATGATTGGGTA (SEQ ID NO: 322) AATTTCAAACCAAATCACC (SEQ ID NO: 323)	461
(SEQ ID NO: 14)	AATTACCAAACCAATTCCTCTTA (SEQ ID NO: 325) GGTTGGGATTTTAGTGTGTG (SEQ ID NO: 324)	366
(SEQ ID NO: 14)	TTATTTGAGGGATTTATTGGAG (SEQ ID NO: 326) CCTTATTAAACTTACCACCCTAT (SEQ ID NO: 327)	382

Name and /or SEQ ID No:	Primer:	Amplifica te Length:
(SEQ ID NO: 15)	GTGGGTTAGTGGGAGGTTAT (SEQ ID NO: 328) TAAAAACCCTTCCTACCTCTTA (SEQ ID NO: 329)	440
(SEQ ID NO: 16)	AGATGGGTATGTATTTTGGGTT (SEQ ID NO: 330) ACTAAACTCAACCACCTCACTAA (SEQ ID NO: 331)	181
(SEQ ID NO: 17)	TTTTGGTTAGTTTTATGGGGTA (SEQ ID NO: 332) CACTACTTCAAATCCATCATCA (SEQ ID NO: 333)	484
LYSOSOMAL- ASSOCIATED MULTITRANSMEMBR NE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TAACTTCACAAATTACCCAACA (SEQ ID NO: 335) AAGAGTGAGGAGTAAGGGAGTT (SEQ ID NO: 334)	455
"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5- PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	TTTTGGGGTTAGTATGTGAGTT (SEQ ID NO: 336) ATCCCAACAACTTCTTCCTC (SEQ ID NO: 337)	482
PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	GAAGAGGAATGGGAAAATTAG (SEQ ID NO: 338) TCACCAACAAAATACCCAA (SEQ ID NO: 339)	500
PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AACCATCAACCATACCTATTTT (SEQ ID NO: 341) TGAGTAAGATGATTATTTGGATTT (SEQ ID NO: 340)	467
(SEQ ID NO: 21)	CACTTCCCACCTCCTTATATC (SEQ ID NO: 343) ATTGGGTTTGAAAGAGTTGTAG (SEQ ID NO: 342)	398
	ATGATGGGAATATGTAAGAATGA	290

Name and /or SEQ ID No:	Primer:	Amplifica te Length:
(SEQ ID NO: 22)	(SEQ ID NO: 344) CTTCTCACTACTAATCTCCTACCC (SEQ ID NO: 345)	
EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILIBRATIVE NITROBENZYLMERCA PTOPURINE RIBOSIDE- SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILIBRATIVE NBMPR-SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES- TYPE (SEQ ID NO: 23)	GAGTTGGAGGGTTTTGTTTTA (SEQ ID NO: 346) CAAACCTCCATAAAATTCATCT (SEQ ID NO: 347)	410
ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	CCACTCACTCAACCCATAA (SEQ ID NO: 349) GTGTGAGGTTTGGGTATTTTT (SEQ ID NO: 348)	398
PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R- PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	GATGGTGGGTAGTGTTGTTTAT (SEQ ID NO: 350) AAAACCTATCTTACCTTTCTCTT (SEQ ID NO: 351)	378
(SEQ ID NO: 26)	ATTCCCACCAAACCTCTAC (SEQ ID NO: 353) AATTAGAGAAGGTTAAATGGGTT (SEQ ID NO: 352)	300

Name and /or SEQ ID No:	Primer:	Amplification Length:
(SEQ ID NO: 27)	AATAACTCCAACCTTTCCTCCC (SEQ ID NO: 355) GGGATTGGGAATTTATTGT (SEQ ID NO: 354)	237
(SEQ ID NO: 27)	GGTGGATGAGTAGTTTGAAGTTT (SEQ ID NO: 356) AAAAACCCCTTTCCTCT (SEQ ID NO: 357)	427
(SEQ ID NO: 28)	GTTGGGGTTTAGTAATTGAAAA (SEQ ID NO: 358) ACCAACACAACTAACACTTACAT (SEQ ID NO: 359)	404
PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN- 14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	AAGAGGTTTTATGGTGTGTTGAG (SEQ ID NO: 360) CACTCCCTTCCCAAACATAC (SEQ ID NO: 361)	473
HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (SEQ ID NO: 30)	CTCCTCAATTCTCACCAAAA (SEQ ID NO: 363) GTGGAAAAGGAGAGTAAATTG (SEQ ID NO: 362)	356
LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK- 1) (SEQ ID NO: 31)	AAACCCTACTTCCTACAAACAA (SEQ ID NO: 365) AGGGAGGTTTGGTGTATTTT (SEQ ID NO: 364)	420
LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II- A) (FC-GAMMA- RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	CAATCCCTTAAAACAAACC (SEQ ID NO: 367) GGAAAGGATAGGATGTTGGAT (SEQ ID NO: 366)	500
1-ACYL-SN- GLYCEROL-3- PHOSPHATE ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1-	CACAATTTCCACAAAACA (SEQ ID NO: 369) TTAGGGAGATGAGATTAAAGGA (SEQ ID NO: 368)	379

Name and /or SEQ ID No:	Primer:	Amplifica te Length:
AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDI C ACID ACYLTRANSFERASE- GAMMA) (LPAAT- GAMMA) (1- ACYLGLYCEROL-3- PHOSPHATE O- ACYLTRANSFERASE 3) (SEQ ID NO: 33)		
HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TATATGGGGTGGGAGTATTTT (SEQ ID NO: 370) CCTTCCCCTCCTTCTTATACT (SEQ ID NO: 371)	276
(SEQ ID NO: 35)	AAAATTCTTTCCTCTCCTAAACA (SEQ ID NO: 373) TTAGGGGTATTAGGTAAATGA (SEQ ID NO: 372)	478
HISTONE H4 (SEQ ID NO: 36)	TTAGTTGAGAAAGTGGGGGT (SEQ ID NO: 374) CTACCTCAAACCAAATCCTC (SEQ ID NO: 375)	421
POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	TTTTGGAGTTATAGGGTTTTGT (SEQ ID NO: 376) CTTCAACATCTCCCAATCC (SEQ ID NO: 377)	441
ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN	AAACCTAAAAATCCAACACAAA (SEQ ID NO: 379) GGGTTATGTTAAGGGAGAAAG (SEQ ID NO: 378)	215

Name and /or SEQ ID No:	Primer:	Amplifica te Length:
ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)		
(SEQ ID NO: 39)	AATAACCTAATCTCCAAACCC (SEQ ID NO: 381) ATTTGTGGTAGTTAATAGGTATGTTTA (SEQ ID NO: 380)	465
(SEQ ID NO: 40)	TACCCACCATATACCAAACTAAA (SEQ ID NO: 383) TAGAGAAGTTGTTTGTGTTG (SEQ ID NO: 382)	484
PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	ATTTGAGGGGTATTATTGTTG (SEQ ID NO: 384) AACCACCTTCTCCCCTAAT (SEQ ID NO: 385)	409
(SEQ ID NO: 42)	GTAATAATTGGGTTAGGGGTTA (SEQ ID NO: 386) AACCAATATCAAATAACTAAAATCC (SEQ ID NO: 387)	394
(SEQ ID NO: 43)	AAAATCCAATCCTAAAACCCTA (SEQ ID NO: 389) TATTTGAGAAAGTGGTAGGAGG (SEQ ID NO: 388)	296
(SEQ ID NO: 44)	AACCCTAACTTCTAACAATTCC (SEQ ID NO: 391) TTTATGTTTGTGGGGGTAGT (SEQ ID NO: 390)	492
(SEQ ID NO: 45)	ACCCCAATCAACTACATAACTAA (SEQ ID NO: 393) GTGAGAGTGGGTGTTGAAAT (SEQ ID NO: 392)	498
(SEQ ID NO: 46)	GAAGGTAGGTTAGTAAGAAGGGT (SEQ ID NO: 394) TACCTAATCCCCCAAACA (SEQ ID NO: 395)	289
(SEQ ID NO: 47)	CACTCACTTAATCATCACCATC (SEQ ID NO: 397) GGAGGAGTTGGGAGTTAGTAT (SEQ ID NO: 396)	459
	TGATTTGATTAGTTTGGTATTGTT	454

Name and /or SEQ ID No:	Primer:	Amplification Length:
(SEQ ID NO: 48)	(SEQ ID NO: 398) CAAACACCCCTTAACCCT (SEQ ID NO: 399)	
(SEQ ID NO: 49)	TAGTGTGTTTGGTTAGAGTGGT (SEQ ID NO: 400) ACACATCTTAAACTTCCCCA (SEQ ID NO: 401)	249
DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	AACCAACACCTCCTAAACAAT (SEQ ID NO: 403) GTTGGGTTTATTTTGAGTTGAG (SEQ ID NO: 402)	412
PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TTGTTTGTTTTGAGTAAGAAGG (SEQ ID NO: 404) ATACCCCAATAACCACCTCTAT (SEQ ID NO: 405)	475
TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	ACCAATCTAAAAATCCCCAAC (SEQ ID NO: 407) GGTATTAGGAGGTAGAAGTGGA (SEQ ID NO: 406)	474
CDH1 (SEQ ID NO: 54)	GAGGTTGGGGTTAGAGGAT (SEQ ID NO: 408)	478

Name and /or SEQ ID No:	Primer:	Amplification Length:
	CAAAC TCACAAATACTTTACAATTC (SEQ ID NO: 409)	
CD44 (SEQ ID NO: 56)	GAAAGGAGAGGTTAAAGGTTG (SEQ ID NO: 410) AACTCACTTAACTCCAATCCC (SEQ ID NO: 411)	696
GSTP1 (SEQ ID NO: 57)	CCTCTCCCCTACCCTATAAA (SEQ ID NO: 413) GTTGGTTTTATGTTGGGAGTT (SEQ ID NO: 412)	469
VIAAT (SEQ ID NO: 59)	CAAACCCAATTCTCAATATCC (SEQ ID NO: 415) GAAGTTGTTGTATATGAGGTTGTTA (SEQ ID NO: 414)	434

TABLE 9

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No:	Gene name and/or SEQ ID NO	Oligo:
1	VIAAT (SEQ ID NO: 59)	TAGACGCGGACGTTTA (SEQ ID NO: 416)
2	VIAAT (SEQ ID NO: 59)	TAATTAGATGTGGATGTT (SEQ ID NO: 417)
3	VIAAT (SEQ ID NO: 59)	TTCGTATAGGTACGCGA (SEQ ID NO: 418)
4	VIAAT (SEQ ID NO: 59)	TTTTGTATAGGTATGTGA (SEQ ID NO: 419)
5	VIAAT (SEQ ID NO: 59)	TTCGTACGCGTATTAT (SEQ ID NO: 420)
6	VIAAT (SEQ ID NO: 59)	GAGTTTTGTATGTGTATT (SEQ ID NO: 421)
7	VIAAT (SEQ ID NO: 59)	TTCGGTCGTTTAGCGT (SEQ ID NO: 422)
8	VIAAT (SEQ ID NO: 59)	ATTTGGTTGTTTAGTGT (SEQ ID NO: 423)
9	(SEQ ID NO: 1)	GTCGGTGGTTCGAGTA (SEQ ID NO: 424)
10	(SEQ ID NO: 1)	GTTGGTGGTTTGAGTAT (SEQ ID NO: 425)
11	(SEQ ID NO: 1)	GGAATTCGACGGGGAG (SEQ ID NO: 426)
12	(SEQ ID NO: 1)	GGGAATTTGATGGGGA (SEQ ID NO: 427)
13	(SEQ ID NO: 1)	TTCGTCGGGCGTTTAG (SEQ ID NO: 428)
14	(SEQ ID NO: 1)	TTTGTGGGTGTTTAGT (SEQ ID NO: 429)
15		GTCGTTTCGTGCATGTA

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 1)	(SEQ ID NO: 430)
16	(SEQ ID NO: 1)	GGTTGTTTGTGATGTAG (SEQ ID NO: 431)
17	(SEQ ID NO: 2)	GTATTGCGCGTTTATT (SEQ ID NO: 432)
18	(SEQ ID NO: 2)	AGGGTATTGTGTGTTTA (SEQ ID NO: 433)
19	(SEQ ID NO: 2)	AGGTACGTGGCGTTTT (SEQ ID NO: 434)
20	(SEQ ID NO: 2)	AGGTATGTGGTGTTTT (SEQ ID NO: 435)
21	(SEQ ID NO: 2)	GAGTTGCGCGGTAGTT (SEQ ID NO: 436)
22	(SEQ ID NO: 2)	AGGAGTTGTGTGGTAG (SEQ ID NO: 437)
23	(SEQ ID NO: 2)	ATAGTTTTCGCGTTTT (SEQ ID NO: 438)
24	(SEQ ID NO: 2)	AGTTTTTGTGTTT TAGGA (SEQ ID NO: 439)
25	(SEQ ID NO: 3)	TTTCGGTCGCGAATAT (SEQ ID NO: 440)
26	(SEQ ID NO: 3)	TTTGTTGTGAATATTTT (SEQ ID NO: 441)
27	(SEQ ID NO: 3)	GTCGAGAGTTCGCGTT (SEQ ID NO: 442)
28	(SEQ ID NO: 3)	TAGTTGAGAGTTTGTGT (SEQ ID NO: 443)
29	(SEQ ID NO: 3)	TTTCGGTACGACGTTT (SEQ ID NO: 444)
30	(SEQ ID NO: 3)	GAGTTTTGGTATGATGT (SEQ ID NO: 445)
31	(SEQ ID NO: 3)	ATTGGGCGCGGTTTAA (SEQ ID NO: 446)
32	(SEQ ID NO: 3)	ATTGGGTGTGGTTTAA (SEQ ID NO: 447)
33	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	ATTGTCGGGATACGTT (SEQ ID NO: 448)
34	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	GATTGTTGGGATATGTT (SEQ ID NO: 449)
35	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	TTAGTGTCGCGTTATT (SEQ ID NO: 450)
36	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	AGTGTTGTGTTATTTGG (SEQ ID NO: 451)
37	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	TGAAACGTTAGCGTTA (SEQ ID NO: 452)
38	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	AGTGAAATGTTAGTGTT (SEQ ID NO: 453)
39	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	AAAGGCGCGGTTTTTA (SEQ ID NO: 454)
40	LIM/HOMEBOX PROTEIN LHX9	TTGAAAGGTGTGTTTT

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 4)	(SEQ ID NO: 455)
41	(SEQ ID NO: 5)	TAAGTAGCGGCGTTGT (SEQ ID NO: 456)
42	(SEQ ID NO: 5)	TAAGTAGTGGTGTGTGA (SEQ ID NO: 457)
43	(SEQ ID NO: 5)	GAGATGAGCGTCGTGG (SEQ ID NO: 458)
44	(SEQ ID NO: 5)	GAGATGAGTGTGTGG (SEQ ID NO: 459)
45	(SEQ ID NO: 5)	GTCGTTTCGTTAGTAACGG (SEQ ID NO: 460)
46	(SEQ ID NO: 5)	GTTGTTTGTGTAGTAATGG (SEQ ID NO: 461)
47	(SEQ ID NO: 5)	TATCGGTTTTTCGCGGT (SEQ ID NO: 462)
48	(SEQ ID NO: 5)	ATATTGGTTTTTGTGGT (SEQ ID NO: 463)
49	(SEQ ID NO: 5)	TTGGACGGCGTGTATT (SEQ ID NO: 464)
50	(SEQ ID NO: 5)	TTTGATGGTGTGTAT (SEQ ID NO: 465)
51	(SEQ ID NO: 6)	GACGTTGTCGTAATGA (SEQ ID NO: 466)
52	(SEQ ID NO: 6)	TGATGTTGTTGTAATGA (SEQ ID NO: 467)
53	(SEQ ID NO: 6)	AGTATACGAGACGCGA (SEQ ID NO: 468)
54	(SEQ ID NO: 6)	AGAGTATATGAGATGTGA (SEQ ID NO: 469)
55	(SEQ ID NO: 6)	TTCGTTTATCGTGCGG (SEQ ID NO: 470)
56	(SEQ ID NO: 6)	TTTGTTTATTGTGTGGT (SEQ ID NO: 471)
57	(SEQ ID NO: 6)	AGGACGTAGAGCGTAG (SEQ ID NO: 472)
58	(SEQ ID NO: 6)	TGAGGATGTAGAGTGT (SEQ ID NO: 473)
59	(SEQ ID NO: 7)	TATAGACGGTGGGCGA (SEQ ID NO: 474)
60	(SEQ ID NO: 7)	TATAGATGGTGGGTGA (SEQ ID NO: 475)
61	(SEQ ID NO: 7)	ATTTATCGCGGTGGTT (SEQ ID NO: 476)
62	(SEQ ID NO: 7)	GGATTATTGTGGTGG (SEQ ID NO: 477)
63	(SEQ ID NO: 7)	ATTCGTTGATTGCGCG (SEQ ID NO: 478)
64	(SEQ ID NO: 7)	TTTGTTGATTTGTGGGG (SEQ ID NO: 479)
65	UBIQUITIN-LIKE PROTEIN SMT3C	TTTAGTCGATTGCGGA

No:	Gene name and/or SEQ ID NO	Oligo:
	PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	(SEQ ID NO: 480)
66	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	AGTTGATTTGGGAGAA (SEQ ID NO: 481)
67	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	TGAGCGAGTTCGGAGA (SEQ ID NO: 482)
68	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	GATGAGTGAGTTTGGA (SEQ ID NO: 483)
69	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	TTTCGGGAGTTTCGTA (SEQ ID NO: 484)
70	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	TTTGGGAGTTTTGTAGT (SEQ ID NO: 485)
71	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1)	TTTCGGTCGTAGTCGG (SEQ ID NO: 486)

No:	Gene name and/or SEQ ID NO	Oligo:
	(UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	
72	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	ATTTTGGTTGTAGTTGG (SEQ ID NO: 487)
73	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATTGAGTTCGGGTTTCGT (SEQ ID NO: 488)
74	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATTGAGTTTGGGTTTGT (SEQ ID NO: 489)
75	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TAGCGTATATGCGATT (SEQ ID NO: 490)
76	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GGGTAGTGTATATGTGA (SEQ ID NO: 491)
77	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATATGCGATTGATTTTACGG (SEQ ID NO: 492)
78	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATATGTGATTGATTTTATGG (SEQ ID NO: 493)
79	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TTATAGCGTCGTATGG (SEQ ID NO: 494)
80	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATAGTGTTGTATGGGAA (SEQ ID NO: 495)
81	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GACGTAGGTTTCGTGAT (SEQ ID NO: 496)
82	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN	ATGATGTAGGTTTGTGA (SEQ ID NO: 497)

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 9)	
83	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GGTAGCGTTTATTCGT (SEQ ID NO: 498)
84	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	AGGTAGTGTTTATTTGTA (SEQ ID NO: 499)
85	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATAGTCGAGTTTCGTT (SEQ ID NO: 500)
86	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GTTGAGTTTTGTTTAGG (SEQ ID NO: 501)
87	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TGGGTATACGTGTTAG (SEQ ID NO: 502)
88	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TATGGGTATATGTGTTAG (SEQ ID NO: 503)
89	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TTAGATGCGTAAGGTT (SEQ ID NO: 504)
90	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATTAGATGTGTAAGGTTT (SEQ ID NO: 505)
91	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TTATGGGTCGTAGGAT (SEQ ID NO: 506)
92	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATGGGTTGTAGGATTG (SEQ ID NO: 507)
93	(SEQ ID NO: 10)	TTCGTTTAGTTACGTACGG (SEQ ID NO: 508)
94	(SEQ ID NO: 10)	TTTGTTTAGTTATGTATGG (SEQ ID NO: 509)
95	(SEQ ID NO: 10)	TAGTTACGTACGGATAT (SEQ ID NO: 510)
96	(SEQ ID NO: 10)	TTATGTATGGATATTTTGG (SEQ ID NO: 511)
97	(SEQ ID NO: 10)	AGGATACGTAGTTCGT (SEQ ID NO: 512)

No:	Gene name and/or SEQ ID NO	Oligo:
98	(SEQ ID NO: 10)	AGGATATGTAGTTTGTATA (SEQ ID NO: 513)
99	(SEQ ID NO: 10)	AGTTCGTATATTTTCGG (SEQ ID NO: 514)
100	(SEQ ID NO: 10)	AGTTTGTATATTTTGGTA (SEQ ID NO: 515)
101	(SEQ ID NO: 11)	TACGGGGTCGTTTCGTA (SEQ ID NO: 516)
102	(SEQ ID NO: 11)	TATGGGGTTGTTTGTAT (SEQ ID NO: 517)
103	(SEQ ID NO: 11)	TTCGTAGGCGATCGTA (SEQ ID NO: 518)
104	(SEQ ID NO: 11)	GATTTGTAGGTGATTGT (SEQ ID NO: 519)
105	(SEQ ID NO: 11)	TAGCGGTCGATTCGTT (SEQ ID NO: 520)
106	(SEQ ID NO: 11)	TAGTGGTTGATTTGTTT (SEQ ID NO: 521)
107	(SEQ ID NO: 11)	GTCGTTACGTTTTTCGG (SEQ ID NO: 522)
108	(SEQ ID NO: 11)	TAGAGTTGTTATGTTTTTGG (SEQ ID NO: 523)
109	(SEQ ID NO: 12)	AAGTTCGTTACGGCGG (SEQ ID NO: 524)
110	(SEQ ID NO: 12)	AGTTTGTTATGGTGGG (SEQ ID NO: 525)
111	(SEQ ID NO: 12)	TACGTTGGTCGACGTT (SEQ ID NO: 526)
112	(SEQ ID NO: 12)	TTTATGTTGGTTGATGT (SEQ ID NO: 527)
113	(SEQ ID NO: 12)	GAGTCGGACGGTGTTT (SEQ ID NO: 528)
114	(SEQ ID NO: 12)	GAGTTGGATGGTGTTT (SEQ ID NO: 529)
115	HOOK2 PROTEIN (SEQ ID NO: 13)	TAGCGTAAAGGGACGAG (SEQ ID NO: 530)
116	HOOK2 PROTEIN (SEQ ID NO: 13)	TAGTGTAAGGGATGAG (SEQ ID NO: 531)
117	HOOK2 PROTEIN (SEQ ID NO: 13)	ATGCGGATATTTTCGTT (SEQ ID NO: 532)
118	HOOK2 PROTEIN (SEQ ID NO: 13)	GGATGTGGATATTTTGT (SEQ ID NO: 533)
119	HOOK2 PROTEIN (SEQ ID NO: 13)	ATTCGTTTTTCGGAGT (SEQ ID NO: 534)
120	HOOK2 PROTEIN (SEQ ID NO: 13)	GGATATTTTGTTTTTGA (SEQ ID NO: 535)
121	HOOK2 PROTEIN (SEQ ID NO: 13)	AGGTAGCGTAAAGGGA (SEQ ID NO: 536)
122	HOOK2 PROTEIN (SEQ ID NO: 13)	AGGTAGTGTAAGGGA (SEQ ID NO: 537)

No:	Gene name and/or SEQ ID NO	Oligo:
123	(SEQ ID NO: 14)	TAACGTATCGTTAGGG (SEQ ID NO: 538)
124	(SEQ ID NO: 14)	AATGTATTGTTAGGGATG (SEQ ID NO: 539)
125	(SEQ ID NO: 14)	TTTTTGGCGCGGAGTA (SEQ ID NO: 540)
126	(SEQ ID NO: 14)	TTTTGGTGTGGAGTAG (SEQ ID NO: 541)
127	(SEQ ID NO: 14)	TAGAGTTCGACGGGTT (SEQ ID NO: 542)
128	(SEQ ID NO: 14)	AGAGTTTGATGGGTTT (SEQ ID NO: 543)
129	(SEQ ID NO: 14)	ATCGAATTATCGGTCGG (SEQ ID NO: 544)
130	(SEQ ID NO: 14)	ATTGAATTATTGTTGG (SEQ ID NO: 545)
131	(SEQ ID NO: 14)	TATTACGGGGAACGGT (SEQ ID NO: 546)
132	(SEQ ID NO: 14)	TATTATGGGGAATGGTT (SEQ ID NO: 547)
133	(SEQ ID NO: 14)	GAACGGTTCGTTTTTA (SEQ ID NO: 548)
134	(SEQ ID NO: 14)	GGGAATGGTTTGTTTT (SEQ ID NO: 549)
135	(SEQ ID NO: 14)	AAGGGGATCGTTTTTT (SEQ ID NO: 550)
136	(SEQ ID NO: 14)	TAAGGGGATTGTTTTTT (SEQ ID NO: 551)
137	(SEQ ID NO: 14)	TTTtagggCGGTTTAA (SEQ ID NO: 552)
138	(SEQ ID NO: 14)	TTAGGGTGGTTTAAGG (SEQ ID NO: 553)
139	(SEQ ID NO: 15)	TGACGAAAATCGATTG (SEQ ID NO: 554)
140	(SEQ ID NO: 15)	GATGAAAATTGATTGGAT (SEQ ID NO: 555)
141	(SEQ ID NO: 15)	GGGTATACGAATACGT (SEQ ID NO: 556)
142	(SEQ ID NO: 15)	GTGGGTATATGAATATGT (SEQ ID NO: 557)
143	(SEQ ID NO: 15)	TTCGAGGTACGGGTT (SEQ ID NO: 558)
144	(SEQ ID NO: 15)	TTTGAGGTATGGGTT (SEQ ID NO: 559)
145	(SEQ ID NO: 15)	TGTTTCGAGGTATATACGT (SEQ ID NO: 560)
146	(SEQ ID NO: 15)	TTGTTTGAGGTATATATGT (SEQ ID NO: 561)
147	(SEQ ID NO: 16)	AGGAGATTCGGTTATAT (SEQ ID NO: 562)

No:	Gene name and/or SEQ ID NO	Oligo:
148	(SEQ ID NO: 16)	GAGGAGATTGTTATAT (SEQ ID NO: 563)
149	(SEQ ID NO: 16)	GTTATTTTCGGTAATGTT (SEQ ID NO: 564)
150	(SEQ ID NO: 16)	AGGTTATTTTGGTAATG (SEQ ID NO: 565)
151	(SEQ ID NO: 16)	TATTAGTCGTTAGTTTGA (SEQ ID NO: 566)
152	(SEQ ID NO: 16)	TATTAGTTGTTAGTTTGAG (SEQ ID NO: 567)
153	(SEQ ID NO: 16)	AGGTTTATACGATAAAGG (SEQ ID NO: 568)
154	(SEQ ID NO: 16)	AGGTTTATATGATAAAGGT (SEQ ID NO: 569)
155	(SEQ ID NO: 17)	TTCGAATATTAGCGCGT (SEQ ID NO: 570)
156	(SEQ ID NO: 17)	ATTTTGAATATTAGTGTGT (SEQ ID NO: 571)
157	(SEQ ID NO: 17)	TTTATGAGCGGCGAGT (SEQ ID NO: 572)
158	(SEQ ID NO: 17)	GAGTGGTGAGTTTAGG (SEQ ID NO: 573)
159	(SEQ ID NO: 17)	AGTCGGTAACGCGTAT (SEQ ID NO: 574)
160	(SEQ ID NO: 17)	AGAGTTGGTAATGTGTA (SEQ ID NO: 575)
161	(SEQ ID NO: 17)	TTTTTTACGCGGAAGG (SEQ ID NO: 576)
162	(SEQ ID NO: 17)	TTTTATGTGGAAGGGG (SEQ ID NO: 577)
163	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	AGGTCGGTCGTAGATA (SEQ ID NO: 578)
164	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	GAGGTTGGTTGTAGAT (SEQ ID NO: 579)
165	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	GACGTTTATTTTCGAGG (SEQ ID NO: 580)
166	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TGATGTTTATTTTGAGGT (SEQ ID NO: 581)

No:	Gene name and/or SEQ ID NO	Oligo:
167	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TTTGATCGGGATGTGA (SEQ ID NO: 582)
168	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TTTGATTGGGATGTGA (SEQ ID NO: 583)
169	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TGTAATTGACGTTTATTT (SEQ ID NO: 584)
170	LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	AATGTAATTGATGTTTATTT (SEQ ID NO: 585)
171	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	ATCGGTGTTAGCGGAT (SEQ ID NO: 586)
172	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	AATTGGTGTAGTGGA (SEQ ID NO: 587)
173	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	ATGTTTCGTAGGTGTCGG (SEQ ID NO: 588)
174	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	TTTGTAGGTGTTGGGTA (SEQ ID NO: 589)
175	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	GTCGTTGTTATCGAGG (SEQ ID NO: 590)
176	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	GGTTGTTGTTATTGAGG (SEQ ID NO: 591)
177	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	ATTGCGGTTTTATCGG (SEQ ID NO: 592)
178	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE)	ATTGTGGTTTTATTGGT (SEQ ID NO: 593)

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 19)	
179	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TTCGATCGGTTGAATA (SEQ ID NO: 594)
180	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TTGAGTTTTGATTGGTT (SEQ ID NO: 595)
181	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAAGTCGCGTAAGGAG (SEQ ID NO: 596)
182	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AAGTTGTGTAAGGAGTA (SEQ ID NO: 597)
183	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGGTTCGTTAATCGTT (SEQ ID NO: 598)
184	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TGAGGTTTGTTAATTGT (SEQ ID NO: 599)
185	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TACGTTGGACGTATAG (SEQ ID NO: 600)
186	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGAGTATGTTGGATGTA (SEQ ID NO: 601)
187	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGTCGCGAGTTATCGA (SEQ ID NO: 602)
188	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGTTGTGAGTTATTGAG (SEQ ID NO: 603)

No:	Gene name and/or SEQ ID NO	Oligo:
189	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAGCGCGTCGTATATA (SEQ ID NO: 604)
190	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	GGAGTAGTGTGTTGTAT (SEQ ID NO: 605)
191	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	GTCGAAAGTCGTTGAG (SEQ ID NO: 606)
192	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	GTTGAAAGTTGTTGAGG (SEQ ID NO: 607)
193	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAGGACGTATCGCGAG (SEQ ID NO: 608)
194	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAGGATGTATTGTGAGT (SEQ ID NO: 609)
195	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGTGTATCGTTTTTCGG (SEQ ID NO: 610)
196	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAGTGTATTGTTTTTTGG (SEQ ID NO: 611)
197	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TTCGTTTACGGTAGTT (SEQ ID NO: 612)
198	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	ATTTTTGTTTATGGTAGTT (SEQ ID NO: 613)
199	PROSTAGLANDIN E2 RECEPTOR, EP4	TGCGTATCGTTAGTTA

No:	Gene name and/or SEQ ID NO	Oligo:
	SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	(SEQ ID NO: 614)
200	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGGTTGTGTATTGTTAG (SEQ ID NO: 615)
201	(SEQ ID NO: 21)	ATTCGGCGAATAGTAG (SEQ ID NO: 616)
202	(SEQ ID NO: 21)	TATTTGGTGAATAGTAGTA (SEQ ID NO: 617)
203	(SEQ ID NO: 21)	ATAGCGTTGGTCGTTA (SEQ ID NO: 618)
204	(SEQ ID NO: 21)	ATAGTGTTGGTTGTTAG (SEQ ID NO: 619)
205	(SEQ ID NO: 21)	TTCGGGATACGAGTTT (SEQ ID NO: 620)
206	(SEQ ID NO: 21)	GTTTGGGATATGAGTTT (SEQ ID NO: 621)
207	(SEQ ID NO: 21)	TACGATAAGTCGGAGA (SEQ ID NO: 622)
208	(SEQ ID NO: 21)	GGGTTATGATAAGTTGG (SEQ ID NO: 623)
209	(SEQ ID NO: 22)	TATCGGCGAGTTGTAT (SEQ ID NO: 624)
210	(SEQ ID NO: 22)	GGTTATTGGTGAGTTG (SEQ ID NO: 625)
211	(SEQ ID NO: 22)	TTAACGTTTGGGGACGT (SEQ ID NO: 626)
212	(SEQ ID NO: 22)	TTAATGTTTGGGGATGT (SEQ ID NO: 627)
213	(SEQ ID NO: 22)	TATTCGCGTTTTTAGAT (SEQ ID NO: 628)
214	(SEQ ID NO: 22)	TTATTTGTGTTTTTAGATTA (SEQ ID NO: 629)
215	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILIBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILIBRATIVE NBMPR-SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE) (SEQ ID NO: 23)	AGGGATAACGGAATATT (SEQ ID NO: 630)
216	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILIBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILIBRATIVE	GAAGGGATAATGGAATAT (SEQ ID NO: 631)

No:	Gene name and/or SEQ ID NO	Oligo:
	NBMPR-SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE (SEQ ID NO: 23)	
217	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILIBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILIBRATIVE NBMPR-SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE (SEQ ID NO: 23)	GAATAGTTTCGAGATGA (SEQ ID NO: 632)
218	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILIBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILIBRATIVE NBMPR-SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE (SEQ ID NO: 23)	GGAATAGTTTTGAGATGA (SEQ ID NO: 633)
219	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TTTTCGACGAAGTTTT (SEQ ID NO: 634)
220	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TTTGTGATGAAGTTTTGTT (SEQ ID NO: 635)
221	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TTACGGAGGCGTTTTA (SEQ ID NO: 636)
222	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR)	TTTTATGGAGGTGTTTT (SEQ ID NO: 637)

No:	Gene name and/or SEQ ID NO	Oligo:
	(HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	
223	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	AGGCGAATTTATCGGG (SEQ ID NO: 638)
224	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	GGTGAATTTATTGGGG (SEQ ID NO: 639)
225	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TAGTCGAAGTAGGCGT (SEQ ID NO: 640)
226	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TAGTTGAAGTAGGTGTT (SEQ ID NO: 641)
227	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	TTCGATCGAAGGTAAT (SEQ ID NO: 642)
228	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	TTTGTGTTGATTGAAGGT (SEQ ID NO: 643)
229	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR)	AGGCGATCGATATTAG (SEQ ID NO: 644)

No:	Gene name and/or SEQ ID NO	Oligo:
	(PHOGRIN) (SEQ ID NO: 25)	
230	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP- X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	GGTGATTGATATTAGGG (SEQ ID NO: 645)
231	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP- X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	TTAGCGTTCGTCGTTA (SEQ ID NO: 646)
232	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP- X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	TAATTAGTGTGTTGTTGTTA (SEQ ID NO: 647)
233	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP- X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	ATCGGTTTCGGGAATTT (SEQ ID NO: 648)
234	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP- X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	AGATTGGTTTGGAAT (SEQ ID NO: 649)
235	(SEQ ID NO: 26)	GTCGATTTCGTTACGG (SEQ ID NO: 650)
236	(SEQ ID NO: 26)	GTTGATTTGTTATGGG (SEQ ID NO: 651)
237	(SEQ ID NO: 26)	TTCGGGTTTCGTATTA (SEQ ID NO: 652)
238	(SEQ ID NO: 26)	TTTTGGGTTTTGTATTAG (SEQ ID NO: 653)
239	(SEQ ID NO: 26)	AATTCGCGGTTTCGAT (SEQ ID NO: 654)
240	(SEQ ID NO: 26)	AATTTGTGTTTTGATG (SEQ ID NO: 655)
241	(SEQ ID NO: 26)	GTCGTTTCGCGGAGAT (SEQ ID NO: 656)
242	(SEQ ID NO: 26)	GTTGTTTTGTGGAGATT (SEQ ID NO: 657)
243	(SEQ ID NO: 27)	ATTGGTCGATTCGCGG (SEQ ID NO: 658)
244		TATTGGTTGATTGTGG

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 27)	(SEQ ID NO: 659)
245	(SEQ ID NO: 27)	AGCGTTTCGATTTCGG (SEQ ID NO: 660)
246	(SEQ ID NO: 27)	AGTGTTTTGATTTTGGT (SEQ ID NO: 661)
247	(SEQ ID NO: 27)	ATCGAGCGTTTCGATT (SEQ ID NO: 662)
248	(SEQ ID NO: 27)	GGATTGAGTGTTTTGAT (SEQ ID NO: 663)
249	(SEQ ID NO: 27)	ATTCGCGTATTCGAGA (SEQ ID NO: 664)
250	(SEQ ID NO: 27)	TTTGTGTATTTGAGAGG (SEQ ID NO: 665)
251	(SEQ ID NO: 27)	GACGTTTCGCGATTAAA (SEQ ID NO: 666)
252	(SEQ ID NO: 27)	TGGATGTTTGTGATTAA (SEQ ID NO: 667)
253	(SEQ ID NO: 27)	AAGTCGATATCGCGGT (SEQ ID NO: 668)
254	(SEQ ID NO: 27)	AAAAGTTGATATTGTGGT (SEQ ID NO: 669)
255	(SEQ ID NO: 27)	AGCGTTTCGGAAGTTTA (SEQ ID NO: 670)
256	(SEQ ID NO: 27)	GGAGTGTTTGGAAGTT (SEQ ID NO: 671)
257	(SEQ ID NO: 27)	TATTCGGACGGGGATA (SEQ ID NO: 672)
258	(SEQ ID NO: 27)	ATTTGGATGGGGATAG (SEQ ID NO: 673)
259	(SEQ ID NO: 27)	GAGACGCGTAGGTTAT (SEQ ID NO: 674)
260	(SEQ ID NO: 27)	GGGAGATGTGTAGGTT (SEQ ID NO: 675)
261	(SEQ ID NO: 28)	TAGTTTTTCGGCGAAGG (SEQ ID NO: 676)
262	(SEQ ID NO: 28)	GGTAGTTTTTGGTGAAG (SEQ ID NO: 677)
263	(SEQ ID NO: 28)	AAGGCGGTGACGTAAA (SEQ ID NO: 678)
264	(SEQ ID NO: 28)	AAGGTGGTGATGTAAA (SEQ ID NO: 679)
265	(SEQ ID NO: 28)	ATGGCGTAAGTACGTT (SEQ ID NO: 680)
266	(SEQ ID NO: 28)	GATGGTGTAAGTATGTT (SEQ ID NO: 681)
267	(SEQ ID NO: 28)	AGTACGTTTCGGGACGA (SEQ ID NO: 682)
268	(SEQ ID NO: 28)	AAGTATGTTTGGGATGA (SEQ ID NO: 683)
269	PEROXISOMAL MEMBRANE PROTEIN	ATGGTATTCGGGTCGT

No:	Gene name and/or SEQ ID NO	Oligo:
	PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	(SEQ ID NO: 684)
270	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TATGGTATTTGGGTTGT (SEQ ID NO: 685)
271	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TTGGAGCGTTAAGTAA (SEQ ID NO: 686)
272	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TATTTGGAGTGTTAAGTA (SEQ ID NO: 687)
273	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TGAAAGATTCGTTTGT (SEQ ID NO: 688)
274	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	GTGAAAGATTGTTTGTT (SEQ ID NO: 689)
275	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TGTATAACGAGAGGTG (SEQ ID NO: 690)
276	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TGTATAATGAGAGGTGA (SEQ ID NO: 691)
277	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN)	ATGTTTCGGGTATGGA (SEQ ID NO: 692)

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 29)	
278	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	ATGTTTTGGGTATGGA (SEQ ID NO: 693)
279	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	TTTTCGAGGAATTCGT (SEQ ID NO: 694)
280	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	TTTTTTGAGGAATTTGTT (SEQ ID NO: 695)
281	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	ATAGTTTTCGGCGGGT (SEQ ID NO: 696)
282	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	TATAGTTTTTGGTGGGT (SEQ ID NO: 697)
283	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	TTTTTCGGCGTAGATA (SEQ ID NO: 698)
284	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	TGTTTTTTTGGTGTAGAT (SEQ ID NO: 699)
285	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	TTACGGGCGTTAGAGA (SEQ ID NO: 700)
286	HOMEBOX PROTEIN HOX-B6 (HOX- 2B) (HOX-2.2) (SEQ ID NO: 30)	GGAGTTATGGGTGTTA (SEQ ID NO: 701)
287	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	TATCGGATTATCGCGG (SEQ ID NO: 702)
288	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	ATTGGATTATTGTGGGG (SEQ ID NO: 703)
289	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	GTCGGTAGTTTATCGGAT (SEQ ID NO: 704)
290	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	GTTGGTAGTTTATTGGAT (SEQ ID NO: 705)
291	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	TAGGAGACGTTACGTT (SEQ ID NO: 706)
292	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	AGATGTTATGTTAGGGT (SEQ ID NO: 707)
293	LOW AFFINITY IMMUNOGLOBULIN	AAGAACGGACGTGTTT

No:	Gene name and/or SEQ ID NO	Oligo:
	GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	(SEQ ID NO: 708)
294	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	AGGAAGAATGGATGTG (SEQ ID NO: 709)
295	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	TTTTTGCGATAGTCGG (SEQ ID NO: 710)
296	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	GTTTTTGTGATAGTTGG (SEQ ID NO: 711)
297	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	TAGCGGCGATTTAAGG (SEQ ID NO: 712)
298	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	GTAGTGGTGATTTAAGG (SEQ ID NO: 713)
299	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	TTTACGAGCGAGTCGT (SEQ ID NO: 714)
300	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A)	TTTTATGAGTGAGTTGTT (SEQ ID NO: 715)

No:	Gene name and/or SEQ ID NO	Oligo:
	(FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	
301	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT- GAMMA) (1-ACYLGLYCEROL-3- PHOSPHATE O- ACYLTRANSFERASE 3) (SEQ ID NO: 33)	TTTCGATAGTATACGGG (SEQ ID NO: 716)
302	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT- GAMMA) (1-ACYLGLYCEROL-3- PHOSPHATE O- ACYLTRANSFERASE 3) (SEQ ID NO: 33)	TTTGATAGTATATGGGGA (SEQ ID NO: 717)
303	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT- GAMMA) (1-ACYLGLYCEROL-3- PHOSPHATE O- ACYLTRANSFERASE 3) (SEQ ID NO: 33)	AAGGGAGCGTTCGTTA (SEQ ID NO: 718)
304	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT- GAMMA) (1-ACYLGLYCEROL-3- PHOSPHATE O- ACYLTRANSFERASE 3) (SEQ ID NO: 33)	AAGGGAGTGTTTGTTA (SEQ ID NO: 719)
305	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT- GAMMA) (1-ACYLGLYCEROL-3-	AATAATAGCGACGGGG (SEQ ID NO: 720)

No:	Gene name and/or SEQ ID NO	Oligo:
	PHOSPHATE O- ACYLTRANSFERASE 3) (SEQ ID NO: 33)	
306	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT- GAMMA) (1-ACYLGLYCEROL-3- PHOSPHATE O- ACYLTRANSFERASE 3) (SEQ ID NO: 33)	TAATAGTGATGGGGT (SEQ ID NO: 721)
307	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTAGAATCGTCGAGT (SEQ ID NO: 722)
308	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	AGAATTGTTGAGTGAAG (SEQ ID NO: 723)
309	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTTTTCGTCGGTTCGTA (SEQ ID NO: 724)
310	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTTGTTGGTTTGTAGGA (SEQ ID NO: 725)
311	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	AGGACGGCGTTTATTA (SEQ ID NO: 726)
312	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	GATGAGGATGGTGTGT (SEQ ID NO: 727)
313	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTCGATTTTCGGAGGAT (SEQ ID NO: 728)
314	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTTGATTTTGAGGATT (SEQ ID NO: 729)
315	(SEQ ID NO: 35)	TTCGTTATCGAGAGTT (SEQ ID NO: 730)
316	(SEQ ID NO: 35)	GGGTTTTGTTATTGAGA (SEQ ID NO: 731)
317	(SEQ ID NO: 35)	GACGTGAGCGTTTAGG (SEQ ID NO: 732)
318	(SEQ ID NO: 35)	GATGTGAGTGTTTAGGG (SEQ ID NO: 733)
319	(SEQ ID NO: 35)	TACGGAGTTGGCGTTA (SEQ ID NO: 734)
320	(SEQ ID NO: 35)	TTTATGGAGTTGGTGT (SEQ ID NO: 735)
321	(SEQ ID NO: 35)	TTGGTTCGTCGAGGAT (SEQ ID NO: 736)
322	(SEQ ID NO: 35)	TTGGTTTGTTGAGGAT (SEQ ID NO: 737)
323	HISTONE H4 (SEQ ID NO: 36)	ATCGAAATCGTAGAGG (SEQ ID NO: 738)
324	HISTONE H4 (SEQ ID NO: 36)	ATTGAAATTGTAGAGGG (SEQ ID NO: 739)
325	HISTONE H4	TATGGCGGTGATCGTT

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 36)	(SEQ ID NO: 740)
326	HISTONE H4 (SEQ ID NO: 36)	TTTATGGTGGTGTGATTGT (SEQ ID NO: 741)
327	HISTONE H4 (SEQ ID NO: 36)	TTACGGCGTTTCGGAT (SEQ ID NO: 742)
328	HISTONE H4 (SEQ ID NO: 36)	TTATGGTGTTTTGGATT (SEQ ID NO: 743)
329	HISTONE H4 (SEQ ID NO: 36)	ATGCGTTTTACGTCGT (SEQ ID NO: 744)
330	HISTONE H4 (SEQ ID NO: 36)	AGATGTGTTTTATGTTGT (SEQ ID NO: 745)
331	HISTONE H4 (SEQ ID NO: 36)	TAAGGCGTCGGATGGT (SEQ ID NO: 746)
332	HISTONE H4 (SEQ ID NO: 36)	GAGTAAGGTGTTGGAT (SEQ ID NO: 747)
333	HISTONE H4 (SEQ ID NO: 36)	TATTTTACGGTGGCGT (SEQ ID NO: 748)
334	HISTONE H4 (SEQ ID NO: 36)	ATTTTATGGTGGTGT (SEQ ID NO: 749)
335	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	ATTTCGGAGGTATCGT (SEQ ID NO: 750)
336	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	TTTGGAGGTATTGTGT (SEQ ID NO: 751)
337	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	TTCGTACGGGGTATAG (SEQ ID NO: 752)
338	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	GGTTTGTATGGGGTATA (SEQ ID NO: 753)
339	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	TATAAGGCGTTACGGT (SEQ ID NO: 754)
340	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	GGTATAAGGTGTTATGG (SEQ ID NO: 755)
341	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2	TTACGGTCGCGTAGTA (SEQ ID NO: 756)

No:	Gene name and/or SEQ ID NO	Oligo:
	(NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	
342	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	TATGGTTGTGTAGTAGT (SEQ ID NO: 757)
343	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	TTATTCGTAGTTTTTCGG (SEQ ID NO: 758)
344	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	GTTTATTTGTAGTTTTTGG (SEQ ID NO: 759)
345	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	TGTAATCGTTTATTCGT (SEQ ID NO: 760)
346	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22)	TAATTGTTTATTTGTAGTTT (SEQ ID NO: 761)

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 38)	
347	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	TTCGAAGTCGGGATTA (SEQ ID NO: 762)
348	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	ATTTTGAAGTTGGGATT (SEQ ID NO: 763)
349	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	ATCGAGAGTATTTCTGAAG (SEQ ID NO: 764)
350	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	GGATTGAGAGTATTTTGA (SEQ ID NO: 765)
351	(SEQ ID NO: 39)	TAAGCGGTATAAGTCGG (SEQ ID NO: 766)
352	(SEQ ID NO: 39)	AGTGGTATAAGTTGGTT (SEQ ID NO: 767)
353	(SEQ ID NO: 39)	TTCGGTAAGCGGTATA (SEQ ID NO: 768)

No:	Gene name and/or SEQ ID NO	Oligo:
354	(SEQ ID NO: 39)	ATAATTTGGTAAGTGGTA (SEQ ID NO: 769)
355	(SEQ ID NO: 39)	TTCGTGATTTTACGTTA (SEQ ID NO: 770)
356	(SEQ ID NO: 39)	AATTTTGTGATTTTATGTT (SEQ ID NO: 771)
357	(SEQ ID NO: 39)	TGGCGACGAAGTGTA (SEQ ID NO: 772)
358	(SEQ ID NO: 39)	TTTGTGGTGATGAAGT (SEQ ID NO: 773)
359	(SEQ ID NO: 40)	TAGCGGGTTTACGGAG (SEQ ID NO: 774)
360	(SEQ ID NO: 40)	AGTAGTGGGTTTATGG (SEQ ID NO: 775)
361	(SEQ ID NO: 40)	TAACGAGTCGAGCGGA (SEQ ID NO: 776)
362	(SEQ ID NO: 40)	AATGAGTTGAGTGGAG (SEQ ID NO: 777)
363	(SEQ ID NO: 40)	TTTTCGCGTGTAAGTT (SEQ ID NO: 778)
364	(SEQ ID NO: 40)	TTTTTGTGTGTAAGTTAA (SEQ ID NO: 779)
365	(SEQ ID NO: 40)	TAGGACGATTCGGATA (SEQ ID NO: 780)
366	(SEQ ID NO: 40)	AGGATGATTTGGATAGT (SEQ ID NO: 781)
367	(SEQ ID NO: 40)	TTCGAGTGAAAGCGGTA (SEQ ID NO: 782)
368	(SEQ ID NO: 40)	TTTGAGTGAAAGTGGTA (SEQ ID NO: 783)
369	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TTACGTTTTTCGTGAAAT (SEQ ID NO: 784)
370	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TTTTATGTTTTTGTGAAAT (SEQ ID NO: 785)
371	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	GGGAGGACGTAGAGTA (SEQ ID NO: 786)
372	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	GGGAGGATGTAGAGTA (SEQ ID NO: 787)

No:	Gene name and/or SEQ ID NO	Oligo:
373	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TGGGTTATCGTTTATATT (SEQ ID NO: 788)
374	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TTGGGTTATTGTTTATATT (SEQ ID NO: 789)
375	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TGGTATCGGTTTTTGAA (SEQ ID NO: 790)
376	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TGGTATTGGTTTTTGAA (SEQ ID NO: 791)
377	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	GTTTAGGTTTCGAGTTTA (SEQ ID NO: 792)
378	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	GGTTTAGGTTTGAGTTTA (SEQ ID NO: 793)
379	(SEQ ID NO: 42)	AGAATTGCGACGGTTT (SEQ ID NO: 794)
380	(SEQ ID NO: 42)	AATTGTGATGGTTTGTA (SEQ ID NO: 795)
381	(SEQ ID NO: 42)	TTACGTTTATTTACGGG (SEQ ID NO: 796)
382	(SEQ ID NO: 42)	TATGTTTATTTATGGGGAT (SEQ ID NO: 797)
383	(SEQ ID NO: 42)	TGGATGTGCGGAAGAA (SEQ ID NO: 798)
384	(SEQ ID NO: 42)	GATGTGTGGAAGAAGT (SEQ ID NO: 799)
385	(SEQ ID NO: 42)	ATGGGTACGTTGTTTA (SEQ ID NO: 800)
386	(SEQ ID NO: 42)	TATGGGTATGTTGTTTAT (SEQ ID NO: 801)
387	(SEQ ID NO: 42)	GGATATTTGCGTTAGTA (SEQ ID NO: 802)
388	(SEQ ID NO: 42)	GGATATTTGTGTTAGTATT (SEQ ID NO: 803)
389		GACGTGTTTCGGGTTTAA

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 43)	(SEQ ID NO: 804)
390	(SEQ ID NO: 43)	GATGTGTTTGGGTTTTA (SEQ ID NO: 805)
391	(SEQ ID NO: 43)	AGTCGACGGTTTGAGG (SEQ ID NO: 806)
392	(SEQ ID NO: 43)	AGTTGATGGTTTGAGG (SEQ ID NO: 807)
393	(SEQ ID NO: 43)	TTATTGCGTTGTTAAGT (SEQ ID NO: 808)
394	(SEQ ID NO: 43)	GTTATTGTGTTGTTAAGT (SEQ ID NO: 809)
395	(SEQ ID NO: 44)	ATTTAAACGGGGTCGT (SEQ ID NO: 810)
396	(SEQ ID NO: 44)	AATTAAATGGGGTTGT (SEQ ID NO: 811)
397	(SEQ ID NO: 44)	ATCGGTTTTTTGTATCGAATA (SEQ ID NO: 812)
398	(SEQ ID NO: 44)	ATTGGTTTTTTGTATTGAATA (SEQ ID NO: 813)
399	(SEQ ID NO: 44)	TTCGGCGTTTTTCGTAG (SEQ ID NO: 814)
400	(SEQ ID NO: 44)	TGAAAGTTCGGCGTTT (SEQ ID NO: 815)
401	(SEQ ID NO: 44)	TTTGGTGTTTTTGTAGG (SEQ ID NO: 816)
402	(SEQ ID NO: 44)	TGAAAGTTTGGTGTTTT (SEQ ID NO: 817)
403	(SEQ ID NO: 45)	ATCGGTTTTTCGAGGT (SEQ ID NO: 818)
404	(SEQ ID NO: 45)	ATTGGTTTTTTGAGGTT (SEQ ID NO: 819)
405	(SEQ ID NO: 45)	GGTCGATTTTCGCGTA (SEQ ID NO: 820)
406	(SEQ ID NO: 45)	TGGTTGATTTTTGTGTA (SEQ ID NO: 821)
407	(SEQ ID NO: 46)	GGTAATTTTCGCGTATT (SEQ ID NO: 822)
408	(SEQ ID NO: 46)	TTGGTAATTTTGTGTATTT (SEQ ID NO: 823)
409	(SEQ ID NO: 47)	TATGCGTATACGTGGT (SEQ ID NO: 824)
410	(SEQ ID NO: 47)	ATGTGTATATGTGGTTTT (SEQ ID NO: 825)
411	(SEQ ID NO: 47)	GTCGTTTTATGCGTAT (SEQ ID NO: 826)
412	(SEQ ID NO: 47)	TGGTTGTTTTATGTGTAT (SEQ ID NO: 827)
413	(SEQ ID NO: 47)	TAGTTTTTCGAATTTTCGT (SEQ ID NO: 828)
414		ATTAGTTTTTGAATTTTGT

No:	Gene name and/or SEQ ID NO	Oligo:
	(SEQ ID NO: 47)	(SEQ ID NO: 829)
415	(SEQ ID NO: 48)	TAGCGAGGGTCGTTTT (SEQ ID NO: 830)
416	(SEQ ID NO: 48)	TAGTGAGGGTTGTTTT (SEQ ID NO: 831)
417	(SEQ ID NO: 48)	TTAGGTCGCGTCGGTA (SEQ ID NO: 832)
418	(SEQ ID NO: 48)	AGGTTGTGTTGGTAGA (SEQ ID NO: 833)
419	(SEQ ID NO: 48)	ATTTCGTTTACGTCGT (SEQ ID NO: 834)
420	(SEQ ID NO: 48)	GGATTTTGTATTATGTTGT (SEQ ID NO: 835)
421	(SEQ ID NO: 48)	TTTTCGTATTCGGGTA (SEQ ID NO: 836)
422	(SEQ ID NO: 48)	TTTGTATTTGGGTAAAAG (SEQ ID NO: 837)
423	(SEQ ID NO: 48)	AGGATCGGGATTCGTA (SEQ ID NO: 838)
424	(SEQ ID NO: 48)	AGGATTGGGATTTGTAG (SEQ ID NO: 839)
425	(SEQ ID NO: 48)	TTCGTTTAAGCGGGGT (SEQ ID NO: 840)
426	(SEQ ID NO: 48)	TTTGTTTAAGTGGGGT (SEQ ID NO: 841)
427	(SEQ ID NO: 49)	ATATTCGTGCGGTCGG (SEQ ID NO: 842)
428	(SEQ ID NO: 49)	ATATTTGTGTGGTTGGA (SEQ ID NO: 843)
429	(SEQ ID NO: 49)	TTAGGTCGTGGAATGT (SEQ ID NO: 844)
430	(SEQ ID NO: 49)	TTAGGTTGTGGAATGT (SEQ ID NO: 845)
431	(SEQ ID NO: 49)	AGGAATCGTGAGTAGG (SEQ ID NO: 846)
432	(SEQ ID NO: 49)	AGGAATTGTGAGTAGG (SEQ ID NO: 847)
433	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTCGATATCGAGTCGG (SEQ ID NO: 848)
434	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	ATTGATATTGAGTTGGT (SEQ ID NO: 849)
435	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	ATTCGCGTTTTAACGT (SEQ ID NO: 850)
436	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTTGTGTTTAAATGTGGA (SEQ ID NO: 851)
437	DNA REPLICATION FACTOR; DOUBLE	TTCGGTTGGGACGTAA

No:	Gene name and/or SEQ ID NO	Oligo:
	PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	(SEQ ID NO: 852)
438	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTTGATTGGGATGTAA (SEQ ID NO: 853)
439	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTAAGGCGTTTAGCGA (SEQ ID NO: 854)
440	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTTTAAGGTGTTTAGTGA (SEQ ID NO: 855)
441	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TATCGTCGAGTGTGTA (SEQ ID NO: 856)
442	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	GGGGTTATTGTTGAGT (SEQ ID NO: 857)
443	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TATTATTCGAGTTAGAGG (SEQ ID NO: 858)
444	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TTATTATTTGAGTTAGAGG (SEQ ID NO: 859)
445	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	AGGATTCGTTGAAGAA (SEQ ID NO: 860)
446	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	GTAGGATTTGTTGAAGA (SEQ ID NO: 861)
447	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TTATTAGGCGATATTTTAA (SEQ ID NO: 862)
448	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TATTAGGTGATATTTTAAGT (SEQ ID NO: 863)
449	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	TAGTACGTTGGTTCGG (SEQ ID NO: 864)
450	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION	TATGTTGGTTTGGAGT (SEQ ID NO: 865)

No:	Gene name and/or SEQ ID NO	Oligo:
	1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	
451	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	AGTTGTTTCGATGATTAG (SEQ ID NO: 866)
452	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	TTTAGTTGTTTGATGATTA (SEQ ID NO: 867)
453	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	AGATTAGTACGTTGGTT (SEQ ID NO: 868)
454	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5;	AAGATTAGTATGTTGGTT (SEQ ID NO: 869)

No:	Gene name and/or SEQ ID NO	Oligo:
	P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	
455	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	TTAAAGCGGGGAGTTT (SEQ ID NO: 870)
456	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	GTTTAAAGTGGGGAGT (SEQ ID NO: 871)
457	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	AGATGGTATCGTTTAGG (SEQ ID NO: 872)
458	TUMOR SUPPRESSING	ATGGTATTGTTTAGGTG

No:	Gene name and/or SEQ ID NO	Oligo:
	SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	(SEQ ID NO: 873)
459	CDH1 (SEQ ID NO: 54)	TATCGCGTTTATGCGA (SEQ ID NO: 874)
460	CDH1 (SEQ ID NO: 54)	ATTGTGTTTATGTGAGG (SEQ ID NO: 875)
461	CDH1 (SEQ ID NO: 54)	TTATGCGAGGTCGGGT (SEQ ID NO: 876)
462	CDH1 (SEQ ID NO: 54)	TTATGTGAGGTTGGGT (SEQ ID NO: 877)
463	CDH1 (SEQ ID NO: 54)	TTAATTAGCGGTACGG (SEQ ID NO: 878)
464	CDH1 (SEQ ID NO: 54)	AATTAGTGGTATGGGG (SEQ ID NO: 879)
465	CDH1 (SEQ ID NO: 54)	TAGTGGCGTCGGAATT (SEQ ID NO: 880)
466	CDH1 (SEQ ID NO: 54)	TAGTGGTGTTGGAATT (SEQ ID NO: 881)
467	CDKN2a (SEQ ID NO: 55)	GGCGTTGTTTAACGTAT (SEQ ID NO: 882)
468	CDKN2a (SEQ ID NO: 55)	GGGTGTTGTTTAATGTA (SEQ ID NO: 883)
469	CDKN2a (SEQ ID NO: 55)	TGTTTAACGTATCGAAT (SEQ ID NO: 884)
470	CDKN2a (SEQ ID NO: 55)	GTTGTTTAATGTATTGAAT (SEQ ID NO: 885)
471	CDKN2a (SEQ ID NO: 55)	AATAGTTACGGTCGGA (SEQ ID NO: 886)
472	CDKN2a (SEQ ID NO: 55)	AGTTATGTTTGGAGGT (SEQ ID NO: 887)
473	CDKN2a (SEQ ID NO: 55)	GTCGGAGGTCGATTTA (SEQ ID NO: 888)
474	CDKN2a (SEQ ID NO: 55)	GTTTGGAGGTTGATTTA (SEQ ID NO: 889)
475	CD44 (SEQ ID NO: 56)	AGGTATTTTCGCGATAT (SEQ ID NO: 890)
476	CD44 (SEQ ID NO: 56)	AGGTATTTTGTGATATTTT (SEQ ID NO: 891)
477	CD44 (SEQ ID NO: 56)	TAGGTTCCGGTTCGTTAT (SEQ ID NO: 892)

No:	Gene name and/or SEQ ID NO	Oligo:
478	CD44 (SEQ ID NO: 56)	TAGGTTTGGTTTGTATT (SEQ ID NO: 893)
479	CD44 (SEQ ID NO: 56)	GTTCGTTTCGGATATTA (SEQ ID NO: 894)
480	CD44 (SEQ ID NO: 56)	TTTGTTTTGGATATTATGG (SEQ ID NO: 895)
481	CD44 (SEQ ID NO: 56)	TTTGCGTAGATCGGT (SEQ ID NO: 896)
482	CD44 (SEQ ID NO: 56)	TTTGGTGTAGATTGGT (SEQ ID NO: 897)
483	CD44 (SEQ ID NO: 56)	TTTAGCGCGGATTTCGG (SEQ ID NO: 898)
484	CD44 (SEQ ID NO: 56)	GTTTAGTGTGGATTTGG (SEQ ID NO: 899)
485	GSTP1 (SEQ ID NO: 57)	ATCGTTGCGATTTCGG (SEQ ID NO: 900)
486	GSTP1 (SEQ ID NO: 57)	ATTGTTGTGATTTTGA (SEQ ID NO: 901)
487	GSTP1 (SEQ ID NO: 57)	AGTGTGCGTAGCGAAT (SEQ ID NO: 902)
488	GSTP1 (SEQ ID NO: 57)	GTGTGTAGTGAATTGG (SEQ ID NO: 903)
489	GSTP1 (SEQ ID NO: 57)	GAGTCGTCGCGTAGTT (SEQ ID NO: 904)
490	GSTP1 (SEQ ID NO: 57)	GGAGTTGTTGTGTAGTT (SEQ ID NO: 905)
491	GSTP1 (SEQ ID NO: 57)	ATTTTCGTCGTTTATAG (SEQ ID NO: 906)
492	GSTP1 (SEQ ID NO: 57)	GGATTTTTGTTGGTTTTA (SEQ ID NO: 907)
493	GSTP1 (SEQ ID NO: 57)	TTCGCGGTTTTTCGAGT (SEQ ID NO: 908)
494	GSTP1 (SEQ ID NO: 57)	TTTGTGGTTTTTGAGTT (SEQ ID NO: 909)
495	GSTP1 (SEQ ID NO: 57)	TAGCGAAGTTTCGCGG (SEQ ID NO: 910)
496	GSTP1 (SEQ ID NO: 57)	AGTGAAGTTTTGTGGT (SEQ ID NO: 911)
497	GSTP1 (SEQ ID NO: 57)	GTCGCGCGTATTTATT (SEQ ID NO: 912)
498	GSTP1 (SEQ ID NO: 57)	GGGTTGTGTGTATTTAT (SEQ ID NO: 913)
499	IGF2 (SEQ ID NO: 58)	TACGTATAAAATTCGTATT (SEQ ID NO: 914)
500	IGF2 (SEQ ID NO: 58)	AAATTATGTATAAAATTTGT (SEQ ID NO: 915)
501	IGF2 (SEQ ID NO: 58)	ATAGACGCGAGTTCGG (SEQ ID NO: 916)
502	IGF2 (SEQ ID NO: 58)	AGATGTGAGTTTGGTT (SEQ ID NO: 917)

No:	Gene name and/or SEQ ID NO	Oligo:
503	IGF2 (SEQ ID NO: 58)	TATCGGGGTGCGTTTA (SEQ ID NO: 918)
504	IGF2 (SEQ ID NO: 58)	ATTGGGGTGTGTTTAA (SEQ ID NO: 919)
505	IGF2 (SEQ ID NO: 58)	TTACGGAGGTTTCGGT (SEQ ID NO: 920)
506	IGF2 (SEQ ID NO: 58)	TTATGGAGGTTTGGT (SEQ ID NO: 921)
507	AR (SEQ ID NO: 53)	TTATAGTCGTAGTCGGT (SEQ ID NO: 922)
508	AR (SEQ ID NO: 53)	AGTTGTAGTTGGTTTG (SEQ ID NO: 923)
509	AR (SEQ ID NO: 53)	GTCGTGGTCGTTAGTA (SEQ ID NO: 924)
510	AR (SEQ ID NO: 53)	GTTGTGGTTGTTAGTAA (SEQ ID NO: 925)
511	AR (SEQ ID NO: 53)	TATTTTCGGACGAGGA (SEQ ID NO: 926)
512	AR (SEQ ID NO: 53)	AGTATTTTGGATGAGG (SEQ ID NO: 927)

EXAMPLE 4

In the following analysis the methylation status of the genes according to Table 10 were analysed by means of methylation specific polymerase chain reaction using the primers according to Table 10 (below).

The study was run on 50 prostate cancer and 50 Benign Prostate Hyperplasia (BPH) tissue samples. Genomic DNA was analyzed using the MSP technique after bisulfite conversion. The bisulfite process converts unmethylated cytosines to uracil while methylated cytosines remained conserved. Bisulfite treatment was performed with minor modifications according to the protocol described in Olek et al. (1996). Sequences of interest were then amplified by means of methylation specific primers, and the amplicate is detected by means of Taqman probes (see Table 10).

TABLE 10

Genomic SEQ ID NO:	Primer	Primer	Taqman probe
20	Cgcgctactccgcat aca (SEQ ID NO: 958)	Gaggtaatcgaggcggt cg (SEQ ID NO: 959)	56- FAM/cgcccaattcatagc cgcacc/3BHQ (SEQ ID

			NO: 960)
36	Accgaaaatacgttc cacg (SEQ ID NO: 961)	Gcgttatcgtaaagtat tgcgc (SEQ ID NO: 962)	/56- FAM/cgcgacgaacaaaac gccg/3BHQ_1/ (SEQ ID NO: 963)
36	Gcgttttacgtcgtc gcg (SEQ ID NO: 964)	Gacgctaaacgccaccg t (SEQ ID NO: 965)	/56- FAM/ccgaccatccgacgc cttactcg/3BHQ_1/ (SEQ ID NO: 966)
51	Cgaattttataccgaa cgctcctacg (SEQ ID NO: 967)	Aggttacgggaggtcga ggtcg (SEQ ID NO: 968)	56-FAM/ cccgccatcgaccgttccc gacccta/3BHQ (SEQ ID NO: 969)
51	Tcccgaattttataacc gaacg (SEQ ID NO: 970)	Ttttatttaggggtcgg gaac (SEQ ID NO: 971)	56-FAM/ acgccccgccatcgaccg/ 3BHQ_1 (SEQ ID NO: 972)
24	Ttgtggttcgggaag agac (SEQ ID NO: 973)	Cttcgatcgaaaaaac cg (SEQ ID NO: 974)	56-FAM/ aactacgcgcaaaccgcg a/3BHQ (SEQ ID NO: 975)
31	Cgtttttcggttttat tttcgc (SEQ ID NO: 976)	Gacaaaaaacgccacgt c (SEQ ID NO: 977)	56- FAM/ccgacaattcacgga atcacgc/3BHQ_1 (SEQ ID NO: 978)
11	Atctcacctaccgtc gcg (SEQ ID NO: 979)	Taggagtgcgatcgttt gc (SEQ ID NO: 980)	56- FAM/acgaacgttacgacc gatacccaacta/3BHQ (SEQ ID NO: 981)
4	Aacgtatcccgacaa tccg (SEQ ID NO: 982)	Gagtattttaagggttag tgaaacgtagc (SEQ ID NO: 983)	56-FAM/ caaataacgcgacactaaa cgcataattc/3BHQ_1 (SEQ ID NO: 984)
4	Tgttttcggagtgcg ttc (SEQ ID NO: 985)	Aaatcaaaccgacgata cga (SEQ ID NO: 986)	56-FAM/ ccgataaaacgcgtccaaa ccg/3BHQ (SEQ ID NO: 987)

The term BHQ denotes Black Hole Quencher (BHQ™) dyes, FAM is a commonly used fluorophore dye molecule.

Reagents:

- 5 A standard set of reagent and cycling conditions are used for MSP establishment and template amplification. Standard conditions are outlined in Tables 11 & 12. Prior to running biological samples, amplicons were established using 100 picograms of completely methylated DNA as a positive control and 100 nanograms of unmethylated DNA as a negative control. Reaction conditions were also checked for relative sensitivity using 50 picograms of methylated
- 10 DNA in a background of 50 nanograms of unmethylated DNA. Reagent concentrations are outlined in Table 11 and cycling conditions for the ABI 7700 are defined in Table 12.

TABLE 11: Reagent concentrations.

Reagent	Stock Conc. (μ M)	Final Rx Conc. (nM)	MM Conc. (μ M)	MM Volume (μ L)
Forward	10.0	500.0	3.33	35.0
Reverse	10.0	500.0	3.33	35.0
Probe	100.0	400.0	2.67	2.8
Water	-	-	-	32.2
Taqmix	-	-	-	245.0
Total	-	-	-	350.0

TABLE 12: Cycling conditions

Temperature (C)	Time (sec)	# of Cycles
Denature		1
95	600	
Annealing		50
95	10	
60 or 63	45	

Data analysis:

Class prediction by supervised learning

In order to give a reliable estimate of how well the CpG ensemble of a selected marker can differentiate between different tissue classes we can determine its prediction accuracy by classification. For that purpose we calculate a methylation profile-based prediction function using a certain set of tissue samples with a specific class label. This step is called training and it exploits the prior knowledge represented by the data labels. The prediction accuracy of that function is then tested on a set of independent samples. As a method of choice, we use the support vector machine (SVM) algorithm (see e.g. Cristiannini, N. and Shawe-Taylor, J. An introduction to support vector machines. Cambridge, UK: Cambridge University Press, 2000.; Duda, R. O., Hart, P. E., and Stork, D. G. Pattern Classification. New York: John Wiley & Sons, 2001.) to learn the prediction function. For this report, sensitivity and specificity are weighted equally. This is achieved by setting the risk associated with false positive and false negative classifications to be inversely proportional to the respective class sizes. Therefore sensitivity and specificity of the resulting classifier can be expected to be approximately equal. Note that this weighting can be adapted according to the clinical requirements.

Results

To determine sensitivity and specificity of said markers, 50 prostate cancer and 50 BPH samples were screened using the defined parameters. Samples had been pre-screened following a technical criterion of methylated DNA vs. unmethylated DNA. After ensuring they were specific for methylated DNA while not amplifying common unmethylated DNA, assays were run using MethyLight realtime PCR on a TaqMan platform (ABI7900). Final assay performance is outlined in Table 13. AUC and corresponding sensitivity and specificity values were calculated using the SVM algorithms.

TABLE 13

Gene name	Genomic SEQ ID NO:	AUC	Sensitivity	Specificity
			Y	Y
PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE	20	0,92 1	0,829	0,871
HISTONE H4	36	0,91 8	0,88	0,719

PR-DOMAIN ZINC FINGER PROTEIN 16	51	0,87 1	0,768	0,822
ORPHAN NUCLEAR RECEPTOR NR5A2	24	0,85 9	0,694	0,878
LIM DOMAIN KINASE 1	31	0,86 8	0,791	0,755
Genomic region	11	0,84 2	0,815	0,704
LIM/HOMEBOX PROTEIN LHX9	4	0,74 5	0,695	0,653

EXAMPLE 5

The objective of the following study was to analyze the methylation status of prostate cancer markers in different body fluid samples in order to identify the preferred choice of body fluid (urine or serum) for testing and the preferred marker, markers or combinations of markers. The study was run on matched serum and urine sediment samples from 80 patients with an average age of 65 and representative of a number of racial types (caucasian, african american etc.). In each case, genomic DNA was analyzed using the HeavyMethyl or MSP technique after bisulfite conversion.

Urine Sediment was prepared for analysis and bisulphite treated according to the following:

- 200 ul sediment samples were purified using the Magnapure DNA Isolation Kit 1 with a 100 ul elution volume.
- 5 ul HD6 PCR was carried out on the Magnapure Eluate, in order to determine DNA concentration
- 100 ul of the DNA solution was treated using the bisulfite treatment technique
- 10 ul C3 bisulfite specific quantitative PCR
- 5 ul 'Merck sulfite test'

Serum was prepared for analysis and bisulphite treated according to the following:

- 1 mL serum samples were purified using the Magnapure DNA Large Volume Total nucleic acid with a 100 ul elution volume.
- 5 ul HD6 PCR on Magnapure Eluate - To determine DNA concentration

- 100 ul of the DNA solution was treated using a proprietary bisulfite treatment technique
- 10 ul C3 bisulfite specific quantitative PCR
- 5 ul 'Merck sulfite test'

HD6 is a genomic assay that amplifies non-bisulfite converted DNA. It is used to
5 quantitate DNA after the initial extraction. It is specific for the beta-globulin gene.

C3 is a bisulfite specific assay located near exon 4 of the GSTP1 gene. It was used in a
fashion similar to our HB14 assay which is also used to quantitate bisulfite converted DNA.

Both require the use of a standard curve and then location of amplification curves and
corresponding concentration is used to give a quantitative value for DNA samples.

10 Single PCR runs were performed on 10 ul of bisulfite treated DNA per sample for each
of the markers as described below.

Heavy Methyl Assay of the GSTP1 gene

15 In the following analysis the methylation status of the gene GSTP1 was analysed by
means of methylation specific amplification using the primers according to Table 1 (below).

The sequence of interest is amplified by means of methylation specific primers and a
blocker oligonucleotide in order to minimise the unspecific amplification of non methylated
DNA. The amplicate is then detected by means of methylation specific Lightcycler probes.

TABLE 14: Oligonucleotides for HeavyMethyl™ – Lightcycler™ analysis of GSTP1.

SEQ ID NO:	Sequence	Type
988	gggattatTTTTtataagggtt	primer
989	ctctaaaccccatcccc	primer
990	cccatccccaaaaacacaaaccac	blocker
991	CGtCGtCGtAGTtTTCGtt-fluo	probe
992	red640-tAGTGAGTACGCGCGGtt-pho	probe

20 Reaction conditions:

PCR program

denat at 95°C

95°C

10min

50 cycles: ramp
denat at 95°C 10 sec (1°C/s)
annealing 56°C 30 sec (1°C/s) detection
extension 72°C 10 sec (1°C/s)

MSP analysis of the gene HISTONE H4.

In the following analysis the methylation status of the gene HISTONE H4 was analysed by means of methylation specific amplification using the primers according to Table 15 (below).

5 The sequence of interest is amplified by means of methylation specific primers, the
amplificate is then detected by means of methylation specific Taqman probes

TABLE 15: Oligonucleotides for MSP – Tagman analysis of HISTONE H4.

SEQ ID NO :	Sequence	Type
993	accgaaaatacgcttcacg	primer
994	gcgttatcgtaaagtattgcgc	primer
995	/56-FAM/cgcgacgaacaaaacgccg/3BHQ_1/	probe

10 Reaction Conditions:

PCR program

denat at 95°C

95°C 10min

50 cycles: ramp
denat at 95°C 10 sec (20°C/s)
annealing 60°C 45 sec (20°C/s) detection

MSP analysis of the gene PROSTAGLANDIN E2 RECEPTOR.

In the following analysis the methylation status of the gene PROSTAGLANDIN E2 RECEPTOR was analysed by means of methylation specific amplification using the primers according to Table 16 (below).

The sequence of interest is amplified by means of methylation specific primers, the
5 amplificate is then detected by means of methylation specific Taqman probes.

TABLE 16A: Oligonucleotides for MSP – Taqman analysis of PROSTAGLANDIN E2 RECEPTOR

SEQ ID NO :	Sequence	Type
996	cgcgctactccgcataca	primer
997	gaggtaatcgaggcggtcg	primer
998	/56-FAM/cgccaattcatacgccgcacc/3BHQ_1/	probe

PCR program

denat at 95°C

95°C 10min

50 cycles:

ramp

denat at 95°C 10 sec (20°C/s)

annealing 60°C 45 sec (20°C/s) detection

10

MSP analysis of the gene ORPHAN NUCLEAR RECEPTOR NR5A2.

In the following analysis the methylation status of the gene ORPHAN NUCLEAR RECEPTOR NR5A2 was analysed by means of methylation specific amplification using the primers according to Table 16(below).

15 The sequence of interest is amplified by means of methylation specific primers, the amplificate is then detected by means of methylation specific Taqman probes.

TABLE 16B: Oligonucleotides for MSP – Taqman analysis of ORPHAN NUCLEAR RECEPTOR NR5A2.

SEQ ID NO :	Sequence	Type
999	ttgtggttcgggaagagac	primer

1000	tcccgaactcttcgatcg	primer
1001	aactacgcgcaaaccgcga	probe

PCR program

denat at 95°C

95°C 10min

50 cycles:

ramp

denat at 95°C 10 sec (20°C/s)

annealing 60°C 45 sec (20°C/s) detection

Marker Analysis

Results were analyzed qualitatively by scoring amplification as +/- and quantitatively by determining the percentage of methylated DNA as a fraction of total DNA calculated using the C3 bisulfite specific PCR. To measure total methylated DNA, a 100% methylated standard (chemicon SSS1 treated DNA) standard curve was included in each assay.

Results

For each marker a Receiver Operating Characteristic curve (ROC curve) of the assay was determined. A ROC is a plot of the true positive rate against the false positive rate for the different possible cutpoints of a diagnostic test. It shows the tradeoff between sensitivity and specificity depending on the selected cutpoint (any increase in sensitivity will be accompanied by a decrease in specificity). The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test (the larger the area the better, optimum is 1, a random test would have a ROC curve lying on the diagonal with an area of 0.5; for reference: J.P. Egan. Signal Detection Theory and ROC Analysis, Academic Press, New York, 1975).

AUC results:

Serum:

Marker: HeavyMethyl GSTP1

AUC: 0.51

Marker: MSP HISTONE H4

AUC: 0.59

Marker: MSP PROSTAGLANDIN E2 RECEPTOR

AUC: 0.52

Marker: MSP ORPHAN NUCLEAR RECEPTOR NR5A2

AUC: 0.50

5

Urine:

Marker: HeavyMethyl GSTP1

AUC: 0.58

Marker: MSP HISTONE H4

10 AUC: 0.5

Marker: MSP PROSTAGLANDIN E2 RECEPTOR

AUC: 0.49

Marker: MSP ORPHAN NUCLEAR RECEPTOR NR5A2

AUC: 0.56

15

To provide an accurate detection of prostate cancer it is preferred that a combined analysis of multiple markers is carried out (i.e. a gene panel). For analysis of urine based samples a preferred combination of markers is GSTP1 , PROSTAGLANDIN E2 RECEPTOR & ORPHAN NUCLEAR RECEPTOR NR5A2 with a sensitivity of 0.37 and a specificity of 0.72.

20 For analysis of serum based samples a most preferred combination of markers is GSTP1 , HISTONE H4 & ORPHAN NUCLEAR RECEPTOR NR5A2 with a sensitivity of 0.35 and a specificity of 0.75.

MSP analysis of the genes according to Table 18.

25 In the following analysis the methylation status of a selection of the genes according to Table 18 were analysed by means of MSP TaqMan assays using the primers and probes according to Table 6 (below).

30 The study was run on 10 samples from prostate carcinoma tissue, 10 from benign prostate hyperplasia tissue and 5 normal prostate tissue samples. Genomic DNA was analyzed using the MSP technique after bisulfite conversion. Total genomic DNA of all samples was bisulfite treated converting unmethylated cytosines to uracil. Methylated cytosines remained conserved. Bisulfite treatment was performed with minor modifications according to the protocol described in Olek et al. (1996).

The sequence of interest was then amplified by means of primers specific for bisulfite treated DNA and the amplicates were detected by means of TaqMan probes using TaqMan and/or Lightcycler platforms. Results are shown in Table 20 below.

Reagents and cycling conditions were as follows:

5

SEQ ID NO: 20

Reagent	Final Conc.
Forward Primer	0.5 uM
Reverse Primer	0.5 uM
Probe	0.4 uM
MgCl	2.5 mM
FastStart	1x
Water	-
Template	-
Total	-

Temperature (C)	Time (sec)	Rate (C/sec)	Collect ?	# of Cycles
Denature				1
95	600	20		
Annealing				50
95	10	20		
60	45	20	single	
Cool				1
40	30	20		

SEQ ID NO: 36

Reagent	MM Volume (uL)
Forward Primer	35.0
Reverse Primer	35.0
Probe	2.8
Water	32.2
Taqmix	245.0
Total	350.0

Temperature (C)	Time (sec)	# of Cycles
Denature		1
95	600	
Annealing		50
95	10	
60	45	

5 SEQ ID NO: 31

Reagent	Final Conc.
Forward Primer	0.5 uM
Reverse Primer	0.5 uM
Probe	0.4 uM

MgCl	2.5 mM
FastStart	1x
Water	-
Template	-
Total	-

Temperature (C)	Time (sec)	Rate (C/sec)	Collect ?	# of Cycles
Denature				1
95	600	20		
Annealing				50
95	10	20		
60	45	20	single	
Cool				1
40	30	20		

5 SEQ ID NO: 11

Reagent	MM Volume (uL)
Forward Primer	35.0
Reverse Primer	35.0
Probe	2.8
Water	32.2
Taqmix	245.0

Total	350.0
--------------	-------

Temperature (C)	Time (sec)	# of Cycles
Denature		1
95	600	
Annealing		50
95	10	
60	45	

5

TABLE 19

Genomic sequence SEQ ID NO:	Forward primer SEQ ID NO:	Reverse primer SEQ ID NO:	Probe SEQ ID NO:
20	1002	1003	1004
36 (assay 4)	1005	1006	1007
36 (assay 1)	1008	1009	1010
31	1011	1012	1013
11	1014	1015	1016

TABLE 20

Genomic sequence SEQ ID NO:	Sensitivity (%)	Specificity
20	70	88
36 (assay 1)	60	94
31	80	80
11	80	79
36 (assay 4)	60	98

10

EXAMPLE 6

Introduction

The GSTPi gene is one of the best characterized methylation prostate diagnostic markers. The aim of the following investigation is to identify methylation markers prostate diagnostic which are able to identify prostate cancers which do not present aberrant GSTPi methylation. It is anticipated that said identified markers would be particularly useful as a member of a gene panel comprising GSTPi for the diagnosis and/or screening of prostate cancers.

Genome wide methylation analysis experiments were carried out to identify differentially methylated sequence candidates among sub-types of prostate cancers, which had different DNA methylation profiles for the *GSTP1* gene. The genome wide methylation analysis methods AP-PCR and MCA were utilized in this study. Three comparisons were run using AP-PCR and two comparisons using MCA as described in the experimental plan.

Comparisons were carried out as the protocols as described in Example 1 above.

Experimental Plan

Four (4) sample pools were used for this study:

Pool #	Sample Nature	Pool Short Name	Sample Size per Pool	Comment
1	Prostate Cancer GSTP1 positive	GSTP1 (+)	12	used for APPCR and MCA

2	Prostate Cancer GSTP1 negative	GSTP1 (-)	2	used for APPCR and MCA
3	Prostate Cancer GSTP1 negative	GSTP1 (-)	4	used for MCA only
4	Prostate Cancer GSTP1 maybe expressed	GSTP1 (?)	2	used for APPCR only

For AP-PCR, 3 sample pools (Pool #1, 2 & 4) were run together to allow a multi-way comparison. Three comparisons were made: GSTP1(+) vs. GSTP1(-), GSTP1(+) vs. GSTP1(?), and GSTP1(-) vs. GSTP1(?). On the same gel, differentially methylated bands migrating at the same speed were assumed to have the same sequences and were, therefore, only cloned and sequenced once. However, every differentially methylated band was assigned a unique MeST ID.

Two MCA comparisons were performed. Both used the GSTP1 (+) sample pool (Pool # 1) as the tester and GSTP1 (-) sample pool (Pool #2 or Pool #3) as driver.

Experimental Results Overview

- 96 non-redundant differentially methylated sequences were identified
- 39 out of the 96 was identified by AP-PCR
- 57 out of the 96 was identified by MCA
- 61 of the non-redundant differentially methylated sequences scored 0 or greater
- None appeared using both methods

Scoring by Method:

Score	0	1	2	3	4	5
AP-PCR	0	9	10	10	3	2
MCA	2	13	9	1	1	1
Total	2	22	19	11	4	3

Interesting Candidate Differentially Methylated Sequences:

The 96 differentially methylated sequences were rated using the following parameters:

5 *% repeat* - percentage of repeat in 1000bp flanking region on either 3' or 5' side of differentially methylated sequences;

% CpG island - percentage of CpG island flanking either side of differentially methylated sequences;

10 *Within promoter* - differentially methylated sequences is found within 5000 bp upstream of exon 1;

Within gene - differentially methylated sequence is found anywhere between flanking exons

 Of these SEQ ID Nos. 1017 to 1028 were selected for further analysis, of particular interest was SEQ ID NO: 1023. SEQ ID Nos. 1017 to 1028 were further investigated by means
15 of sensitive assays according to Example 7 below.

EXAMPLE 7

Introduction

20 In the following analysis the methylation status of the genes according to Table 21 were analysed by means of methylation specific polymerase chain reaction, using the method and samples as described in Example 4.

25 The study was run on 50 prostate cancer and 50 Benign Prostate Hyperplasia (BPH) tissue samples. Genomic DNA was analyzed using the MSP technique after bisulfite conversion. The bisulfite process converts unmethylated cytosines to uracil while methylated cytosines remained conserved. Bisulfite treatment was performed with minor modifications according to the protocol described in Olek et al. (1996). Sequences of interest were then amplified by means of methylation specific primers, and the amplicate is detected by means of Taqman probes (see Table 21).

30

TABLE 21

Genomic SEQ	Forward Primer	Reverse Primer	Probe SEQ
-------------	----------------	----------------	-----------

ID NO:	SEQ ID NO:	SEQ ID NO:	ID NO:
1017	1077	1078	1079
1024	1080	1081	1082
1027	1083	1084	1085
1018	1086	1087	1088
1019	1089	1090	1091
1021	1092	1093	1094
1023	1095	1096	1097
1023	1098	1099	1100
1025	1101	1102	1103
1028	1104	1105	1106
1026	1107	1108	1109
1020	1110	1111	1112
1116	1113	1114	1115
18	1179	1180	1181

Results:

Statistical methods used are as described above in Example 4.

5

TABLE 24: Sensitivity and specificity of MSP assays

Gene	ROC AUC	SVM Acc	SVM Sens	SVM Spec
SEQ ID NO:1023	0,953	0,898	0,888	0,908
RASSF1a.Nelson	0,903	0,828	0,800	0,857
SEQ ID NO:1028	0,809	0,762	0,742	0,783
SEQ ID NO:1113	0,629	0,561	0,527	0,557
SEQ ID NO:1025	0,579	0,561	0,240	0,896
SEQ ID NO:1020	0,561	0,567	0,599	0,534
SEQ ID NO:1019	0,532	0,527	0,869	0,171
SEQ ID NO:1027	0,512	0,499	0,895	0,088
SEQ ID NO: 18	0,533	0,491	0,803	0,167

EXAMPLE 8

Panels

The best performing markers in terms of assay based performance as deduced from Examples 1 to 7 above are shown in Table 25.

In order to optimise the performance of markers in the detection of prostate cancer MSP assays of markers according to Examples 4 and 7 above were combined in gene panels of 2 and 3. Tables 22 to 24 below illustrate the sensitivity and specificity of said combinations of MSP assayed markers in the detection of prostate cancer.

TABLE 22: Sensitivity and specificity of Prostate cancer using MSP assays of 2 markers.

Marker 1	Marker 2	Sensitivity	Specificity
SEQ ID NO: 1023	SEQ ID NO: 57	0,860	0,967
SEQ ID NO: 1023	SEQ ID NO: 20	0,864	0,948
SEQ ID NO: 1023	SEQ ID NO: 4	0,864	0,935
SEQ ID NO: 1028	SEQ ID NO: 1023	0,860	0,938
SEQ ID NO: 1116	SEQ ID NO: 1023	0,860	0,938
SEQ ID NO: 1027	SEQ ID NO: 1023	0,860	0,938
SEQ ID NO: 1019	SEQ ID NO: 1023	0,860	0,938
SEQ ID NO: 1020	SEQ ID NO: 1023	0,860	0,938
SEQ ID NO: 1023	SEQ ID NO: 1025	0,860	0,938
SEQ ID NO: 1023	SEQ ID NO: 11	0,860	0,938
SEQ ID NO: 1023	SEQ ID NO: 24	0,860	0,938
SEQ ID NO: 1023	SEQ ID NO: 18	0,860	0,938
SEQ ID NO: 1023	SEQ ID NO: 31	0,864	0,933
SEQ ID NO: 1023	SEQ ID NO: 35	0,880	0,917
SEQ ID NO: 20	SEQ ID NO: 57	0,812	0,978

TABLE 23: Sensitivity and specificity of Prostate cancer using MSP assays of 3 markers.

Marker 1	Marker 2	Marker 3	Sensitivity	Specificity
SEQ ID NO: 1023	SEQ ID NO: 18	SEQ ID NO: 57	0,86	0,97916667
SEQ ID NO: 1023	SEQ ID NO: 4	SEQ ID NO: 57	0,86	0,97826087
SEQ ID NO: 1116	SEQ ID NO: 1023	SEQ ID NO: 57	0,86	0,975
SEQ ID NO: 1020	SEQ ID NO: 1023	SEQ ID NO: 57	0,864	0,97083333
SEQ ID NO: 1028	SEQ ID NO: 1023	SEQ ID NO: 57	0,86	0,97083333
SEQ ID NO: 1027	SEQ ID NO: 1023	SEQ ID NO: 57	0,864	0,96666667
SEQ ID NO: 1023	SEQ ID NO: 57	RASSF1a	0,86	0,97021277
SEQ ID NO: 1019	SEQ ID NO: 1023	SEQ ID NO: 57	0,86	0,96666667
SEQ ID NO: 1023	SEQ ID NO: 31	SEQ ID NO: 57	0,864	0,9625
SEQ ID NO: 1019	SEQ ID NO: 1023	SEQ ID NO: 20	0,868	0,95652174
SEQ ID NO: 1023	SEQ ID NO: 20	SEQ ID NO: 4	0,88	0,94347826
SEQ ID NO: 1023	SEQ ID NO: 1025	SEQ ID NO: 57	0,852	0,97083333
SEQ ID NO: 1023	SEQ ID NO: 51	SEQ ID NO: 57	0,86	0,9625
SEQ ID NO: 1023	SEQ ID NO: 20	SEQ ID NO: 57	0,86	0,96086957
SEQ ID NO: 1020	SEQ ID NO: 1023	SEQ ID NO: 20	0,868	0,95217391

EXAMPLE 9

In order to provide an alternative assay format to the MSP assays as described above, further HeavyMethyl assays were established. The primers and blockers of said assays are shown in Table 24.

5 Table 24: HeavyMethyl Assay Components

Marker	Primer SEQ ID NO:	Primer SEQ ID NO:	Blocker SEQ ID NO:	Probe SEQ ID NO:	Probe SEQ ID NO:
GSTP1 (assay 1)	1121	1122	1123	1124	1125
GSTP1 (assay 2)	1126	1127	1128	1129	1130
GSTP1 (assay 3)	1131	1132	1133	1134	1135
GSTP1 (assay 4)	1136	1137	1138	1139	1140
SEQ ID NO: 20 (assay 1)	1141	1142	1143	1144	1145
SEQ ID NO: 20 (assay 2)	1146	1147	1148	1149	1150
SEQ ID NO: 24 (assay 1)	1151	1152	1153	1154	1155
SEQ ID NO: 24 (assay 2)	1156	1157	1158	1159	1160
SEQ ID NO: 24 (assay 3)	1161	1162	1163	1164	1165
SEQ ID NO: 36 (assay 1)	1166	1167	1168	1169	1170

GSTP1 LightCycler program:

activation: 95°C 10min

10

50 cycles: 95°C 10 sec (20°C/s)

56°C 30 sec (20°C/s)

72°C 10 sec (20°C/s) detection

15 melting curve: 95°C 10sec 20

40°C 10sec 20

70°C 0sec 0,1

cooling: 40°C 5 sec

5

SEQ ID NO: 20, SEQ ID NO: 24 & SEQ ID NO: 36

LightCycler program:

activation: 95°C 10min

10 55 cycles: 95°C 10 sec (20°C/s)

56°C 30 sec (20°C/s)

72°C 10 sec (20°C/s)

melting

95°C 10sec 20

15 35°C 20sec 20 detection

95°C 0sec 0,1

TABLE 25

20

Marker	ROC AUC	AUC St Err	SVM Acc	SVM Sens	SVM Spec
SEQ ID NO: 1023	0,953	0,000	0,898	0,888	0,908
GSTP1	0,932	0,001	0,928	0,892	0,965
PROSTAGLANDIN E2 RECEPTOR	0,921	0,001	0,849	0,829	0,871
HISTONE H4	0,918	0,001	0,801	0,880	0,719
RASSF1A	0,903	0,001	0,828	0,800	0,857
PR-DOMAIN ZINC FINGER PROTEIN 16	0,871	0,001	0,794	0,768	0,822
LIM DOMAIN KINASE 1	0,858	0,001	0,773	0,791	0,755
ORPHAN NUCLEAR RECEPTOR NR5A2	0,859	0,001	0,784	0,694	0,878
SEQ ID NO: 11	0,842	0,002	0,761	0,815	0,704
SEQ ID NO: 1028	0,809	0,002	0,762	0,742	0,783
LIM/HOMEBOX PROTEIN LHX9	0,745	0,003	0,675	0,695	0,653
SEQ ID NO: 1116	0,629	0,003	0,561	0,527	0,597
SEQ ID NO: 1025	0,579	0,001	0,561	0,240	0,896
SEQ ID NO: 1020	0,561	0,003	0,567	0,599	0,534
LYSOSOMAL-ASSOCIATED	0,533	0,004	0,491	0,803	0,167

MULTITRANSMEMBRANE PROTEIN					
SEQ ID NO: 1019	0,532	0,004	0,527	0,869	0,171
SEQ ID NO: 1027	0,512	0,001	0,499	0,895	0,088

TABLE 26: Genes and sequences according to present invention

Gene ref seq ID:	Genomic SEQ ID NO:	Sense methylated converted SEQ ID NO:	Antisense methylated converted SEQ ID NO:	Sense unmethylated converted SEQ ID NO:	Antisense unmethylated converted SEQ ID NO:
genomic sequence	1	60	61	178	179
genomic sequence	2	62	63	180	181
genomic sequence	3	64	65	182	183
NM_014242	4	66	67	184	185
genomic sequence	5	68	69	186	187
genomic sequence	6	70	71	188	189
genomic sequence	7	72	73	190	191
NM_003352	8	74	75	192	193
NM_003458	9	76	77	194	195
genomic sequence	10	78	79	196	197
genomic sequence	11	80	81	198	199
genomic sequence	12	82	83	200	201
NM_013312	13	84	85	202	203
genomic sequence	14	86	87	204	205
genomic sequence	15	88	89	206	207
genomic sequence	16	90	91	208	209
genomic sequence	17	92	93	210	211
NM_006762	18	94	95	212	213
NM_005539	19	96	97	214	215
NM_000958	20	98	99	216	217
genomic sequence	21	100	101	218	219
genomic sequence	22	102	103	220	221
NM_004955	23	104	105	222	223
NM_003822	24	106	107	224	225
NM_032526	25	108	109	226	227
genomic sequence	26	110	111	228	229
genomic sequence	27	112	113	230	231
genomic sequence	28	114	115	232	233
NM_004565	29	116	117	234	235
NM_156037	30	118	119	236	237

NM_002314	31	120	121	238	239
NM_021642	32	122	123	240	241
NM_020132	33	124	125	242	243
NM_133267	34	126	127	244	245
genomic sequence	35	128	129	246	247
NM_003495	36	130	131	248	249
NM_004518	37	132	133	250	251
NM_003916	38	134	135	252	253
genomic sequence	39	136	137	254	255
genomic sequence	40	138	139	256	257
NM_002705	41	140	141	258	259
genomic sequence	42	142	143	260	261
genomic sequence	43	144	145	262	263
genomic sequence	44	146	147	264	265
genomic sequence	45	148	149	266	267
genomic sequence	46	150	151	268	269
genomic sequence	47	152	153	270	271
genomic sequence	48	154	155	272	273
genomic sequence	49	156	157	274	275
NM_030928	50	158	159	276	277
NM_022114	51	160	161	278	279
NM_002555	52	162	163	280	281
NM_000044	53	164	165	282	283
NM_004360	54	166	167	284	285
NM_000077	55	168	169	286	287
NM_000610	56	170	171	288	289
NM_000852	57	172	173	290	291
NM_000612	58	174	175	292	293
NM_080552	59	176	177	294	295
genomic sequence	1017	1029	1030	1053	1054
genomic sequence	1018	1031	1032	1055	1056
genomic sequence	1019	1032	1034	1057	1058
genomic sequence	1020	1033	1036	1059	1060
genomic sequence	1021	1034	1038	1061	1062
genomic sequence	1022	1035	1040	1063	1064
genomic sequence	1023	1036	1042	1065	1066
genomic sequence	1024	1037	1044	1067	1068
genomic sequence	1025	1038	1046	1069	1070
genomic sequence	1026	1039	1048	1071	1072
genomic sequence	1027	1040	1050	1073	1074
genomic sequence	1028	1041	1052	1075	1076

Genomic sequence	1116	1117	1118	1119	1120
AF102770	1171	1172	1173	1174	1175

Names of genes according to Table 26, wherein the table specifies "Genomic sequence" there is currently no gene mapped to the given sequence.

5

NM_014242:LIM/HOMEODOMAIN PROTEIN LHX9

NM_003352:UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN)

10

NM_003458:"BASSON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN"

NM_013312:HOOK2 PROTEIN

NM_006762:LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5

15

NM_005539:"""TYPE I INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) "

NM_000958:PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

20

NM_004955:EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILIBRATIVE NITROBENZYL MERCAPTOPYRIMIDINE RIBOSIDE-SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILIBRATIVE NBMPR-SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE

NM_003822:ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

25

NM_032526:PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN)

NM_004565:PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14)

30

(PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN)

NM_156037:HOMEODOMAIN PROTEIN HOX-B6 (HOX-2B) (HOX-2.2)

NM_002314:LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1)

NM_021642:LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

NM_020132:1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GAMMA
 5 (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT-GAMMA) (1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

NM_133267:HOMEBOX PROTEIN GSH-2

NM_003495:HISTONE H4

10 NM_004518:POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2)

NM_003916:ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY
 15 PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22)

NM_002705:PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN)

NM_030928:"DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA,
 20 HOMOLOG OF"

NM_022114:PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1)

NM_002555:"TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME
 25 CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN"

NM_000044:AR

30 NM_004360:CDH1

NM_000077:CDKN2a

NM_000610:CD44

NM_000852:GSTP1

NM_000612:IGF2

NM_080552:VIAAT
AF102770:RASSF1A